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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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A Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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1850
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGPPHSGPGGVRVGALLLLG......PVYIVQDGPPQSPPNIYYKV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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1605.064 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10	9	89	7	თ	ហ	4.	ω	2	1	Result
632	632	637.5	637.5	1836	1841	1844	1850	1850	1850	Score
34.2	34.2	34.5	34.5	99.2	99.5	99.7	100.0	100.0	100.0	% Query Match
346	346	336	334	340	455	340	340	340	340	% Query Match Length DB
17	5	17	17	19	18	<u>1</u> 8	18	18	18	BB
AAR91930	AAR55059	AAR92742	AAW00287	AAW46615	AAW33698	AAW17081	AAW10637	AAW31544	AAW33699	SUMMARIES
Human cytokine elk	Elk tyrosine kinas	Murine hepatoma tr	Mouse Eph receptor	Human transmembran	AL-2-long (AL-21)	EPH family ligand	NLERK2 ligand for	Human cytokine Ler	AL-2-short (AL-2s)	Description

Amino acid s	19 AAW71007	200	9 9 V W	172	4 D Q Q
O	AAR9476	200	٠	172	60
	AAB54	218		172.5	47
	AAY0682	213		lП	o,
0	AAW7100	209		176	ίŌ
ы	AAR9476	209		176	4.
Murine LERK-	AAY0682	184	٠	176	Ü
σ	AAR9128	184		176	Ñ
	AAW0258	184		176	ü
Human hek-	AAR7148	238	٠	179	ö
Eph transmembrane	AAR8260	234		181	ø
Drosophi	ABB6554	652		182	æ
Drosophi	ABB5862	652	٠	182	7
Human ephrin B1 C	AAY7143	82		201	õ
Human pancreat	AAB5418	106		202.5	ຫົ
		82		N)	4
3		136	۲	20	ũ
Peptide		136		0	ถ
Human pe		92	'n	9	ñ
Peptide #11708	22 AAM37671	92	15.4	284.5	30
Receptor		195	ω	ŭ	ő
Ligand #1 for rece		195	ω	3	8
Human epi		229	ω	443	7
Murine e		229	4.	447	9
Ephrin-B		683	4	452.5	ĭš
Ephrin-B		8 0 0 0	4	53.	ž.
Human epl		89	9	492	ũ
Ligand fo		308	ü	19.	_{ій}
Ligand #		308	ω	19.	ĭĭ
Receptor-		333	4.	629.5	ŏ
Human LERK-5 cy	AAR8928	333	4.	29.	ō
Human hej		3 3 3	4.	29.	600
Ligand f	AAR9465	333	4	29.	7
Full length	AAW0633	333	4	29.	بو
Chicken	AAW0028	331	4	30.	ភ
Eph transmembrane	AAR8260	346	4.	631	4
Human elk-I	AAW44	346	4.	632	ພັ
	AAW1924	346	4	632	'n
Tuniidi GTA	110 11000				i

ALIGNMENTS

AAW33699;

AAW33699 standard; Protein; 340 AA.

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RESULT 1
AAW33699
ID AAW3
XX AAW3
AC AAW3
AC AAW3
XX AL-2
XX A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour; rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia; psoriasis; Alzheimer's disease; epilepsy.
                                                      WO9740153-A1.
                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                               /note= "signal peptide"
27..340
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                        /note= "extracellular domain"
220..245
                                                                                                                                                             /note= "hydrophobic transmembrane domain"
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301

GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

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Best Local S
Matches 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL-2 can be used as cognitive enhancer, to enhance learning particularly in dementias or trauma, since they can promote axonal outgrowth and synaptic plasticity, particularly of hippocampal neurons that express AL-2 binding Eph-family receptors and cortical neurons that express AL-2. AL-2 can also be used for wound healing, i.e. accelerating neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids are useful in preparing antibodies that specifically bind to the AL-2 protein. The antibodies and the AL-2 antagonists are useful in diagnosing and treating various neuronal disorders. AL-2 antagonists can be used for modulating angiogenesis. They can also be used for the treatment of tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML), myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents, to promote the survival or growth of neurons. They can be used to treat motoneuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and various conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disorders, such as Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome nerve deafness, Menier's disease, and other disorders of the cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human AL-2 neurotrophic factor and related DNA - used to develop products for, e.g. treating neurologic disorders, angiogenesis disorders, tumours or rheumatoid arthritis or for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-535837/49
N-PSDB; AAV06355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related tyrosine kinase receptor ligand. AL-2 can be administered to patients in whom the nervous system has been damaged by trauma, surgery, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Fig 2A-B; 86pp; English.
  301
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                                                                                                                                                                                                                                                                                                                                                                                                        MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
                                                                                                                                                                                                                                                                                                                   LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLICCDRPDLDLRFTIKFQEY 120
                                                                                                                                                                                                                                                                                                                                                                       MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRPQAEGGYVLYPQIGDRLDL 60
GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                         GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGFREAEFGELGIALRGG
                                                                                                                                                        VSEMEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                        SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
                                                                                                                                                                                                                                               SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
                                                                            GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        340;
                                                                                                                          VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 2.9e-143;
); Mismatches 0;
  340
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ARBSULT 2
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This protein sequence comprises a novel human cytokine designated Lerk-8. The amino acid sequence was deduced from a human foetal brain cDNA clone (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk, which are members of the eph/elk family of polypeptides comprising amino acid residues -27 to 142-197 of the cell surface polypeptides comprising amino acid residues -27 to 142-197 of the cell length protein, can be expressed in transformed host cells. These polypeptides can be used to purify hek or elk proteins, and to purify or identify cells that express hek or elk proteins, and to purify or neural cells expressing elk can be aufface. Such cells can be used in various in vitro studies or in vivo procedures, e.g. neural cells expressing elk can be administered to a mammal afflicted with a neurodegenerative disorder. The Lerk-8 collypeptides can also be used to deliver diagnostic or therapeutic agents to these cells (e.g. leukaemia cells). The Lerk-8 DNA and collypeptides can also be used to: treat disorders mediated by collypeptides can also be used to: treat disorders mediated by collypeptides can also be used to flerk-8; to treat disorders such as injury to neural tissue or neurologic disease; to promote such as injury to neural tissue or neurologic disease; to promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-503043/46.
N-PSDB; AAT89519.
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ligand; neurodegenerative disease; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated cytokine, Lerk-8 - binds to the hek and elk receptor tyrosine kinases, used to develop products for diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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210..212
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28..224
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Best Local S
Matches 340
                                         05-FEB-1996;
20-JUL-1995;
27-NOV-1995;
22-DEC-1995;
  Nicola NA;
                                                                                                                                                                                                                                                                                            LERK; ligand for eph-related kinase; ERK; NLERK2; receptor protein tyrosine kinase; cell proliferation; cell differentiation; cell survival; nerve cell.
                                                                                                                                         WO9704091-A1
                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        AAW10637 standard;
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                                                                                                19-JUL-1996;
                                                                                                                     06-FEB-1997.
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                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                          Homo sapiens.
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                       (AMRA-) AMRAD
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les 340; Conservative
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                      OPERATIONS PTY LTD
                                         96AU-0007890.
95AU-0004263.
95AU-0006847.
95AU-0007299.
                                                                                              96WO-AU00460
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/label= Mat_protein
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Pred. No. 2.9e-143;
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AC AAMI
XX AAMI
XX EPH
XX EFH
XX Eff-
XW Liga
XX Liga
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Matches 340
                                                                                                                    Efl-6; I
ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel human ligand for eph-related kinase (LERK) is designated MLERK2 (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human foetal brain cDNA library. The novel receptor ligand can be expressed in transformed host cells and used in methods for regulating the development, maintenance or regeneration of different cells (e.g. neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be used to treat injury, disease or abnormality in the nervous system, and membrane-bound NLERK2 to modulate proliferation, different or survival e.g. in grafting procedures or transplantation. NLERK2 can also be used to raise antibodies for use in immunotherapy, and to detect anti-NLERK2 antibodies that may occur in some autoimmune diseases.
                                                                                   Homo sapiens
                                                                                                                                                                     EPH family
                                                                                                                                                                                                     09-AUG-1997 (first entry)
                                                                                                                                                                                                                                        AAW17081;
                                                                                                                                                                                                                                                                       AAW17081 standard; Protein;
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                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                  Eph; Elk; receptor tyrosine kinase; signal transduction; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 100.0%; Score 1850; DB 18; Similarity 100.0%; Pred. No. 2.9e-143; 40; Conservative 0; Mismatches 0;
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                                                                                                                                                                     ligand Ef1-6.
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1..24
/label= Sig_peptide
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                                                 Location/Qualifiers
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Matches 339
                                                                                                                                                                                                                                                                                                                                                                                                                           A novel ligand (AAM17081), designated Ef1-6 (or Eph transmembrane tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4, Hek and Sek1 receptors on cells. Its amino acid sequence was deduced from a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6, truncated soluble polypeptides comprising the extracellular domain of Elf-6, and Ef1-6 ligandbodies comprising soluble Ef1-6 and the Fc portion of IgG can be expressed in host cells. These can be used to support neuronal and other Eph receptor-bearing cell populations for treatment of neurological disorders, in drug screening and to raise diagnostic
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                       GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                     GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
                                                                                                            VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP
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 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                     VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                    LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPHLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                                                                                                                                                                                                                   339;
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225...249
/label= Transmembrane_domain
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Pred. No. 9e-143; 
0; Mismatches 1;
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RESULT 5
AAW33698
ID AAW3
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AAW33698 standard; Protein; 455

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Query Match Best Local

Similarity

99.5%;

Score 1841; DB 18; Pred. No. 2.2e-142;

Length 455;

Sequence

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CC ischaemia, infection, metabolic disease, nutritional deficiency, cc malignancy, or toxic agents, to promote the survival or growth of ce neurons. They can be used to treat mctoneuron disorders such as ceresis (Lou Gehrig's disease), Bell's palsy, and can be used to treat mctoneuron disorders such as conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disease, such as continuous conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disorders, such as comerve deafness, Menier's disease, and other disorders, such as conerve deafness, Menier's disease, and other disorders of the cerebellum. Cc AL-2 can be used as cognitive enhancer, to enhance learning particularly in dementias or trauma, since they can promote axonal outgrowth and synaptic plasticity, particularly of hippocampal neurons that express Cc AL-2 binding Eph-family receptors and cortical neurons that express AL-2 binding Eph-family receptors and cortical neurons that express Cc AL-2 binding Eph-family receptors and cortical neurons that express Cc AL-2 and also be used for wound healing, i.e. accelerating conditions and the AL-2 antagonists are useful in diagnosing are useful in preparing antibodies that specifically bind to the AL-2 conditating various neuronal disorders. AL-2 antagonists are useful in diagnosing conditating angiogenesis. They can also be used for the treatment of tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML), cmyelodysplastic syndrome (MDS), diabetic retinopathy, neovascular conditions and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human AL-2 neurotrophic factor and related DNA - used to develop products for, e.g. treating neurologic disorders, angiogenesis disorders, tumours or rheumatoid arthritis or for wound healing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine kinase receptor ligand. AL-2 can be administered to patients whom the nervous system has been damaged by trauma, surgery, stroke, ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents, to promote the survival or growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV06354.
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                   Modulating transmembrane ligand for an Elk-related receptor tyrosine kinase - by formation of a complex between an oligomerised Elk-related receptor tyrosine kinase and a transmembrane ligand
                                                                                                                                 N-PSDB; AAV16097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC This polypeptide comprises human Elk-L3, a transmembrane ligand of CC Elk-related receptor tyrosine kinase (ERRTK). A novel method of CC modulating the biological activity of, or for affecting a pathway CC regulated by, a transmembrane ligand for an ERRTK in a cell C expressing the transmembrane ligand for an ERRTK in a cell C expressing the transmembrane ligand for an ERRTK, or an isoform CC or an extracellular domain of the ERRTK, and the transmembrane CC ligand expressed on the cell. The complex can also be used for CC evaluating a substance for its ability to modulate the biological CC evaluating a substance for its ability to modulate the biological CC evaluating a substance for its ability to modulate the biological CC evaluating a substance for its ability to modulate the biological CC evaluating a substance for its ability to modulate by a ERRTK. CC A purified and isolated oligomerised ERRTK can be used in the CC preparation in a subject, or in a medicament for modulating neuronal development or cregeneration in a subject, or in a medicament for modulating conducting can be used to modulate axonogenesis, nerve cell convolving trauma and injury to the nervous system, such as convolving trauma and injury to the nervous system, such as convolving trauma and injury to the nervous system, such as convolving trauma such is part to the nervous system, deficiency diseases, such as multiple sclerosis, amyotrophic CC lateral sclerosis, bacterial and viral infections of the nervous system, deficiency diseases, such as wernicke's disease and conditions convolving trauma such is part to the nervous and infections of the nervous system, deficiency diseases, such as wernicke's disease and conditions convolving to the nervous system, such as mand infections of the nervous system, deficiency diseases, such as wernicke's disease and conditions of the nervous convolving trauma conditions of the nervous system deficiency diseases.
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Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction; organogenesis; oncogenesis; tumour; neurological disorder; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shy Drager's syndrome, cerebellar atrophy, pe
                                                                                      Mouse
                                                                                                                                 19-JAN-1997
                                                                                                                                                                         AAW00287;
                                                                                                                                                                                                                  AAW00287 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                                                                                                                                                                                                                                                                                                                                                              GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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                                                                                   Eph
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                                                                                   receptor ligand
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                                                                                                                              (first entry
                                                                                                                                                                                                                  Protein; 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral nerve damage,
                                                                                   BLF-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1836;
Pred. No. 4e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trauma, and ischaemia
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Best Local Sim
Matches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Eph receptor ligand ELF-2 (AAW00287) is strongly expressed the anterior hindbrain and newly-forming somities of embryos at the early organogenesis stage of development. It is important in cellular communication during pattern formation. Its amino acid sequence was deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain cDNA library. The ELF-2 ligand can be used to alter neurological development, oncogenesis and growth regulation, to modulate binding of ELF-2 to the Eph receptor, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eph receptor ligand, ELF-2, and DNA encoding it - used to prevent neurological diseases, and to modulate binding of Eph receptor, e.g. to prevent or treat tumour formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bergemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic assays.
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                                                                                                                                                                                                                                                                       GLIMVLCRTAISRSIVLEPIYWNSSNGKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 71
                                                                                                                                                                                                                                                                                                  GALLLIGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                  GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1996-433391/43.
                YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                              WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                         GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFÄGIÄSGCIIFIVIIITLVVLLL
                                                                                                                                  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC
                                                                                                                                                             DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 191
                                                                                                                                                                                        DYYLIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                              PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                   KYRRRHRKHSPOHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR--
YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Fig 1A-B; 50pp; English.
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    334
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                    AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Extracellular_domain
31..15
/label= Receptor_binding_site
226..251
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          34.5%;
                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                           Score 637.5; DB 17;
Pred. No. 4.6e-44;
9; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treat
ELF-2
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                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity
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specific typing (partic. as a marker for breast cancer) and as a
marker for human chromosome 13. The ligands (partic. in soluble
form) are used to activate the tyrosine kinase domain of the
Htk receptor, i.e. to stimulate or inhibit growth, differentiation,
and/or activation of cells conty. the receptor, e.g. treatment
of neurodegenerative diseases, since they are strongly expressed
in the cerebral cortex, hippocampus, striatum and cerebellum.
The ligands are also useful as a control or standard in assays,
for generation of antibodies, as a mol. wt. marker, for growth
in vitro of Htk-receptor positive cells, as research agent,
in screening, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse (AAT16470) and human (AAT16471) Htk ligand which activate, the Htk receptor, have been identified in a v tissues using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the murine Htk ligand protein signal peptide cleavage is 34 kD with an estimated pI of the murine and human ligands show 96% homology at the a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stimulating and inhibiting cells cartreating neuro-degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligand for the hepatoma trans-membrane kinase receptor - stimulating and inhibiting cells carrying the receptor, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatoma transmembrane kinase; Htk; tyrosine kinase; neurodegenerative of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH )
134
                             134
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                                                                                                                     17
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                     DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
 DYYTTSTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN
                                                                                        PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                     GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGOGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                                                                                 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Fig 1(A-D); 88pp; English.
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                                                                                                                                                                                                                                            336 AA;
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                                                                                                                                                                                49;
                                                                                                                                                                                Score 637.5; DB 1
Pred. No. 4.6e-44;
9; Mismatches 129
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variety o
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                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                          New DNA encoding ligand for elk tyrosine kinase receptor related polypeptides, vectors, antibodies and probes, use in studying cell differentiation or growth
                                                                                                                                                                                  The sequence is that of the elk-L protein able to bind a tyrosine kinase receptor. The DNA may be incorporated in which can used to study the role of elk and its ligands
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                     Claim 7; Page 30; 35pp;
                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                    Baum PR,
                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elk tyrosine kinase receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1995
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              CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
  CPRAEAGRP----
                                                                        PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                               1994-183415/22.
DB; AAQ65486.
                                                PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYRRRHRKHSPOHTTILSISTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
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                                                                                                  145;
                                                                                                                                                                          and differentiation.
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                             IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
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                                                                                                                                                                                                                                      English.
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                                                                                                            Score 632;
Pred. No. 1
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The present sequence is the human cytokine elk-ligand (elk-L), which binds a member of the tyrosine kinase receptor family. Elk-L exhibits neurotrophic and neuroprotective properties, and has a calculated mol. wt. 35180 daltons and a pI of 9.006. The elk-L cDNA, isolated from a human placental cDNA library, can be radiolabelled and used as a probe for isolating other mammalian elk-L cDNA. Elk-L can be used to treat neural tissue disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor; neurotrophic; neuroprotective; placenta; radiolabelled probe; treatment; neural tissue; excito-toxicity; injury; disorder; neural culture reagent; immunogenic fragment; antibody.
                                                                                                                                                                         WPI; 1996-229866/23.
N-PSDB; AAT28770.
                                                                                                        Claim 1; Columns 27-30; 18pp; English.
                                                                                                                                   probe to
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13-NOV-1992;
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/label= sig_peptide
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Best Loca
Matches
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        Cleavage-site
                          Cleavage-site
                                                                                  Domain
                                                                                                                       Domain
                                                                                                                                        Protein
                                                                                                                                                        Peptide
                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                        extracellular
                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
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domain; i
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                                                                                                                                                                                                      e; ligand; tyrosine kinase receptor; fusion protein;
immunoglobulin; neurological disease.
                                  "Asn
                                                                                        "extracellular domain; this region is used generate a fusion protein with the Fc port of the human immunoglobulin G1"
                                                                                                                               "mature protein"
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                                                                         "transmembrane domain"
                  "KEX2
                                                      "intracellular domain"
"KEX2
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Pred. No. 1.3e-43;
8; Mismatches 116;
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Best Local Similarity
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13-NOV-1992;
02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the human elk-L protein, a new cytokine that is the ligand for the elk tyrosine kinase receptor. The extracellular domain of the protein (amino acids 1-213) is used to generate a fusion protein comprising the rc polypeptide of the human immunoglobulin G1 (extending from the hinge region to the C-terminus). The fusion protein (which has the same activities as the natural elk-L protein) has neuroprotective and neurotrophic activity so is potentiall useful for treating a wide range of neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble fusion proteins of human elk-ligand fragment - and their dimers and oligomers, uneuro-protectants and neurotrophic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Columns 27-30; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baum PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-1995;
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340
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DB; AAT97976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGGVRVGALLLLGVLGLVSGL-----SLEPVYMNSANKRFQAEGGYVLYPQIGDRLDLL
                                                                    STLASPXGGSGTAGTEPSDIIIPLR---TTENNYCHYYEKVSGDYGHPVYIVQEMEPQSP
                                                                                                                                                                                                                                                                                                                                                              CPRABAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQE[RFTIKFQEFS
                                                                                                                                                                                                                                                                                                                                                                                                    CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS
ANIYYKV
                                     PNIYYKV
                                                                                                                                             GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ
                                                                                                                                                                                                                    SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD
                                                                                                                                                                                                                                                      SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                                                                                                                                                                                                                                             PNYMGLEPKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT
                                                                                                                                                                                                                                                                                                                               PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                             PĠQRWLĠKWLVAMVVWALCRLATPLAKNLEPVSWSŚLNPKFLSGKGLVIYPKIGDKLDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMUNEX CORP.
                                                                                                      -GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beckmann MP,
                                                                                                                                                                                 -LLLLGVAGAGGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0213403.
92US-0977693.
95US-0460741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "KEX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 632; DB 18;
Pred. No. 1.3e-43;
8; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ß
                                                                                                                                                                               -----MCWRRRRAKPSESRHPGPGSFGRGGSLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cleavage
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                                                                                                                                               -----RAAALSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potentially
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                                                                                                            333
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standard;

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13-NOV-1992;
01-JUN-1995;
                                                                                                                                                                                                                                                           The present sequence is a human elk ligand (elk-L) protein, which binds elk, has a calculated molecular weight of 35180 and an isoelectric point of 9.006. Blk-L is a cytokine that can be used to test cells for elk expression, measure the biological activity of elk, purify elk by affinity chromatography and as a neuroprotective agent to treat diabetic, hereditary and nutritional neuropathies and neurodegenerative diseases. It may also be added to tissue cultures to prolong the life of neurons. The elk-L cDNA was isolated from a human placental cDNA library, and is present as a cDNA insert in the recombinant vector deposited in strain
                                                                                                                                                                                                                                                                                                                                                                                                                           Human elk ligand protein - as neuro-protective agent
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-271366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; elk; li
purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW19249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5627267-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human elk ligand protien.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nutritional; neuropathy; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                        119
                                                 122
 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                          64
                                                                                                 62
                                                                                                                                                                                      Local Similarity
                                                                                                                          4.
                                                                                                                                                 œ
                                                                                                                                                                                                                                                   insert
69085.
                                                                        CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDENVLVTCNRPEQEIRFTIKFQEFS
                                                                                    CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                        PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR,
                       PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                               PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV
                                                                                                                                               PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                         145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elk; ligand; elk-L; cytokine; testing; measuring;
cation; neuroprotection; treatment; diabetic; hereditary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                culture.
                                                                                                                                                                                                                                                                                                                                                                                                  Columns 29-32; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beckmann MP,
                                                                                                                                                                                                                          346 AA;
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0213403.
92US-0977693.
95US-0458077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= sig_peptide
25..346
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                     34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyman
                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                      for diagnostic
                                                                                                                                                                                     Score 632; DB 18;
Pred. No. 1.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                  English.
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                                                                                                                                                                         Mismatches
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R
                                                                                                                                                                         116;
                                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutic
                                                                                                                                                                                              Length 346;
                                                                                                                                                                         Indels
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                                                                                                                                                                      Gaps
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RESULT 13
AAW44323
AD AAW44
AC AAW44
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-1994;
13-NOV-1992;
02-JUN-1995;
                                             The present sequence represents human elk-L (elk ligand). The present invention describes antibodies to elk-L polypeptides. The elk-L protein is known to be neuroprotective exhibiting its effect through a trophic mechanism. Examples of diseases that may be treated with elk-L include neuropathies e.g. diabetic, hereditary and mutritional neuropathies, neurodegenerative diseases and other diseases characterised by loss of function or degeneration of neurons.
Sequence
                                                                                                                                                                                                                                                              Claim 1; Column 31-32; 17pp; English.
                                                                                                                                                                                                                                                                                                              Antibodies to elk ligand polypeptides - bind receptors, useful for treating neural disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5728813-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; elk-L; elk ligand;
tyrosine kinase receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human elk-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44323 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
                                                                                                                                                                                                                                                                                                                                                                                                  1998-206621/18.
DB; AAV15226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLKKKHRKHTQQ----
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346
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92US-0977693.
95US-0460741.
96US-0747240.
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25..346
/label= elk-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine; antibody; cell surface receptor; neural disease; trophic mechanism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCWRRRAKPSESRHPGPGSFGRGGSLGL
                                                                                                                                                                                                                                                                                                                                             to tyrosine kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333
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Query Match 34.: Best Local Similarity 39.: Matches 145; Conservative

34.2%;

48;

Score 632; DB 19; Pred. No. 1.3e-43; 8; Mismatches 116;

Length 346; Indels

5B •

Gaps

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RESULT 14
AAR82606
ID AAR82
XX AAR82
XX AAR82
XX 16-MA
XX Ef1-2
XX New neuro
XX Homo
X
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                                                                                                                                                                                                                                         21-OCT-1994;
04-APR-1994;
12-APR-1994;
01-SEP-1994;
                                                                                                                   Aldrich TH,
Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
  neurological disorders
                                                                                                                                                                                                                                                                                                                                                                  04-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9527060-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Efl-2; EHKl-L; Eph transmembrane tyrosine kinase family ligand; neurological disorder; identification; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eph transmembrane tyrosine kinase family ligand, Efl-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR82606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR82606 standard;
                       Ligands which bind Eph
                                                                          WPI; 1995-358635/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                              (REGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
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                                                                                                                                                                                              REGENERON
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                                                                                                                      Davis S, GD;
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                                                                                                                                                                                                                                         94US-0327423.
94US-0222075.
94US-0229402.
94US-0299567.
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238..263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "borders main conserved regions"
                                                                                                                                                                                              PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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                       family receptors - used
                                                                                                                                             Gale N,
                                                                                                                                                                                              INC
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                                                                                                                                             Goldfarb M,
                                                                                                                                             Maisonpierre
                         Ë
                         the diagnosis
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ID AAWOO
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AC AAWOO
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Best Local :
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                                                                                                                                                                                                              Gallus sp.
                                                                                                                                                                                                                                       diagnosis;
                                                                                                                                                                                                                                                      Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction;
organogenesis; oncogenesis; tumour; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                          Bergemann AD,
                                                                                                27-FEB-1995;
                                                                                                                           23-FEB-1996;
                                                                                                                                                        06-SEP-1996.
                                                                                                                                                                                                                                                                                               Chicken Eph receptor ligand
                                                                                                                                                                                                                                                                                                                          19-JAN-1997
                                                                                                                                                                                                                                                                                                                                                        AAW00288;
                                                                                                                                                                                                                                                                                                                                                                                  AAW00288 standard; Protein; 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                   WO9626958-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLEPVSWSSLNPXFLSGXGLVIYPXIGDKLDIICPRAEAGRP----YEYYKLYLVRPEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVLLLKLRKRHRKHTQQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----mcwrrrakpsesrhpgpgsfgrggslgl----gggggmgpreaepgelgialrgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGKHETNVQEEKSGP-----GASGGSSGDPDGFFNSKVALFAAVGAGCVIFLLIIIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENREGGVCRTRTMKI IMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQAPGSRGSLGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE-PGKENLPGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                      HARVARD
                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 AA;
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                                          Flanagan
                                                                                                 95US-0395415
                                                                                                                             96WO-US02673
                                                                      COLLEGE
                                                                                                                                                                                                                                       therapy.
                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                 ELF-2.
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Pred. No. 1.6e-43;
4; Mismatches 105;
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WPI; 1996-433391/43 N-PSDB; AAT40231.

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Best Local S
Matches 135
                                                                                                                                                                                                                                                              17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in cellular communication during pattern formation. It is strong expressed in the anterior hindbrain and newly-forming somites of embryos at the early organogenesis stage of development. Its amics sequence was deduced from a cDNA clone (AAT40231) isolated a chicken cDNA library. The ELF-2 ligands can be used to alter neurological development, oncogenesis and growth regulation, to modulate binding of ELF-2 to the Eph receptor, and in diagnostic
                23-JUL-1996
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                 Full length
                                                                                                                                                                                                                                                                                         AAW06337;
                                                                                                                                                                                                                                                                                                                     AAW06337 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eph receptor ligand, ELF-2, and DNA encoding it - used t prevent neurological diseases, and to modulate binding c Eph receptor, e.g. to prevent or treat tumour formation.
                                            JP08188596-A.
                                                                                      Protein
                                                                                                                                                                                                    Receptor-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                         CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNYEFYKLYLYGGAQGRRCEAPPAPNILLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLKYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTNGKSSTTSPFVKDHSGSSTDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER----- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYEYYKVYMVDKDQADSCAIRKDNTPLLNCAKPDQDVKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALMVIMRTALAKSIVIDPIYMNSSNPKFLPGQGLVLYPQIGDKLDIICPKV---DSKTA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331
                                                                                                                                                                                                                                 ligand
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                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                   tyrosine kinase; ligand; coomassie staining; PAS
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                                                                                                                Location/Qualifiers
                                                                                                   note=
                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                            entry)
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40.5%; Pred. No. 1.7e-43;
tive 53; Mismatches 124;
                                                                                                 "signal peptide"
                                                                      "receptor-type tyrosine kinase binding
                                                                                                                                                                                                                              receptor-type tyrosine kinase protein.
                                                                                                                                                                                                                                                                                                                     333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SKAGHSSILGSEVALFAGIASGCIIFIVIIITLVV
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ELF-2
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Best Local
                                                                                                                                             18-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the full length receptor-type tyrosine kinase protein binding ligand of the invention (also see AAW06333 and AAW06334). The mature protein contained within this sequence contains the N-terminal fragment represented by AAW06332. The proteins of the invention have a molecular weight of 23500 (plus or minus 1500) Da, and are positive for Coomassie staining and PAS staining. The proteins of the invention bind to the fragment of this protein sequence represented by AAW06330. The proteins of the invention are new ligands of receptor-type tyrosine kinases, and can be prepared by standard
                                                               haematopoietic
                                                                            Receptor type tyrosine kinase; TK; ligand; differentiation;
                                                                                                          Ligand for receptor type tyrosine kinase (TK).
                                                                                                                                                                                                       AAR94655 standard; Protein; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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N-PSDB; AAT42594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New ligand for receptor type tyrosine kinase - has kilo:dalton(s) and is positive for Coomassie and PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Page 44-46; 51pp; Japanese.
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19-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 GQYEYYKVYMYDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
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                                                                                                                                                                                                                                                                                                                                                                               WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVERKPVSEMEMER-DR
                                                                                                                                                                                                                                                                                     YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                                                                                                 KYRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                                                                                                                                               GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL
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                                                                                                                                                                                                                                                                                                                  YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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                                                                                                                                           (first
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                                                               cell; tyrosine; bone marrow;
                                                                                                                                          entry)
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Pred. No. 2.1e-43;
2; Mismatches 130;
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                                                               leukaemia
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Best Local Sim
Matches 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A ligand polypeptide which binds to the extracellular part of a specific receptor-type tyrosine kinase and induces phosphotylation of tyrosine within the cell can be used in the study of the differentiation of blood cells such as the haematopoietic stem cells; of disease processes such as leukaemia, and of the biology of bone marrow transplantation. The ligand plays a role in the differentiation process and the specific ligand target is expressed in the specific ligand target is expressed to the specific ligand target target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligand peptide binding intracellular tyrosine undifferentiated blood
 Hepatoma transmembrane kinase;
                                 Human hepatoma transmembrane kinase receptor ligand
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07-OCT-1994;
                                                                                                                                AAR92743 standard;
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DB; AAT18395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AA;
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94JP-0244433.
94JP-0262882.
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                                                                                                                                Protein; 333
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Pred. No. 2.1e-43;
2; Mismatches 130
 Htk;
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 receptor; ligand
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Matches
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YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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The DNA is used to produce recombinant ligands, for tissue-
specific typing (partic. as a marker for breast cancer) and as a
marker for human chromosome 13. The ligands (partic. in soluble
form) are used to activate the tyrosine kinase domain of the
Htk receptor, i.e. to stimulate or inhibit growth, differentiation,
and/or activation of cells contg. the receptor, e.g. treatment
of neurodegenerative diseases, since they are strongly expressed
in the cerebral cortex, hippocampus, striatum and cerebellum.
The ligands are also useful as a control or standard in assays,
for generation of antibodies, as a mol. wt. marker, for growth
in vitro of Htk-receptor positive cells, as research agent,
in screening, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activate, the Htk receptor, have been identified in a variety of tissues using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the murine Htk ligand protein following signal peptide cleavage is 34 kD with an estimated pI of 8.9. The protein and human ligands show 96% homology at the amine level.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligand for the hepatoma trans-membrane kinase receptor - useful stimulating and inhibiting cells carrying the receptor, e.g. for treating neuro-degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 2(A-B); 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALLLIGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
KYRRRHRKHSPOHTTTLSLSTLATPKRSGNN----NGSEPSDIIPLR---TÄDSVFCPH
                                                                                                                              GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                           GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC
                                                                                                                                                                                                                                                                                                                                                                                       GOYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
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                                                             WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGFREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                         DYYIISTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                                      DYYITATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                                                                                                                              PNYBFYKLYLVGGAQGRRCBAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHBFRSHH
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Pred. No. 2.1e-43;
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   N-PSDB; AAQ99288
                  WPI; 1996-097585/10
                                                     Cerretti DP,
                                                                                                                       08-JUL-1994;
                                                                                                                                                        06-JUL-1995;
                                                                                                                                                                                           25-JAN-1996.
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276..2
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257..2
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/note= "KEX2 protease processing site"
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GenBank L13189 translation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Soluble LERK-5 (claim 3)"
                                                                                                                                                                                                                                                                                               "KEX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "N-glycosylation
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                                                                                                                                                                                                                                                                                                                              "KEX2 protease processing
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                Key
Peptide
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                                                                     Homo
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                                                                    sapiens
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The sequence represents a full-length LERK-5 cytokine, which binds elk and hek receptor protein-tyrosine-kinases (members of the eph/elk family), and expressed from a gene isolated by amplification with primers specific for a chromosome-13 expressed sequence tag, GenBank L13189, from a human T-lymphocyte leukaemia CCRF-HSB-2 (ATCC CCL L10.1) cell line, followed by cDNA probe screening of a human fetal brain cDNA library in phage lambda-gtl0. A truncated soluble form may also be produced. The protein may be produced as a recombinant fusion protein or dimer with an antibody Fc fragment or e.g. a FLAG affinity tail (R89288). LERK-5 may be used in binding assays to detect elk- or hek-expressing cells, to measure elk or hek activity, as a drug delivery for elk or hek receptor-specific cell therefore, e.g. for delivery of cytostatic agents in leukaemia
Receptor-type tyrosine kinase; LPM medium; ligand; autophosphorylation; insect cell; animal cell; growth promoter; undifferentiated cell; insulin; interleukin; fibroblast growth factor; hepatocyte growth factor; nerve growth factor; interferon-gamma; tumour necrosis factor; inducer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding LERK-5 cytokine capable of binding elk and hek - used as carrier to deliver attached (anti-leukaemic) agents to cells bearing elk or hek, i.e. human leukaemia cell lines JM and LK63
                                                                                                                                Receptor-type
                                                                                                                                                                                                                                                                                               AAW11308 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GALLLIGVIGIVSGISLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLICPRARPPGPHSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                         (first entry)
                                                                                                                                tyrosine kinase #4.
                                                                                                                                                                                                                                                                                             protein;
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Pred. No. 2.1e-43
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/label= signal peptide Location/Qualifiers

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RESULT 21
AAW06334
ID AAW06
XX
XX
AC AAW06
AC TAW06
DT 17-JA
XX
XX
DE Ligar
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAWI1307 and AAWI1308 represent receptor-type tyrosine kinases. These sequences are included in the LPM medium of the invention. The medium is used to culture cells capable of producing a ligand for receptor-type tyrosine kinase. The ligand serves as a physiologically active substance to induce enzyme activity and autophosphorylation of tyrosine kinase, which is involved in the development and differentiation of animal and insect cells. The ligand can also be used as in a pharmaceutical preparation for promoting growth of undifferentiated cells. The medium may also include an inducer, such as insulin, an interleukin, a fibroblast growth factor, or interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                Ligand #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 40-41; 45pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPM cell culture medium - for culture ceptor-type tyrosine kinase ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-APR-1995;
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                                                                                        AAW06334;
                                                                                                                         AAW06334 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALLLIGVIGIVSGISLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1997-014848/02
                                                                                                                                                                                                                                                                                   KYRRRHRKHSPOHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                                                       WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                                                                                                                                                       GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                                                                                                          GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                                                                                                                                                                                              DYYTTSTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                              YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASAHI
                for receptor-type tyrosine kinase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 AA;
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                                                      (first
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            즛
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 629.5; DB 18;
Pred. No. 2.1e-43;
2; Mismatches 130;
                                                                                                                                                                                                                                                 340
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   RESULT 22
AAR94656
ID AAR94
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AC AAR94
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DT 18-OC
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DE Ligar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06333 and AAW06334 represent receptor-type tyrosine kinase receptor binding ligands of the invention. These sequences both have the N-terminal sequence represented by AAW06332. The ligands of the invention recognise the fragment of the receptor type kinase receptor represented by AAW06330 (see AAW06331 for full length sequence). The proteins of the invention have a molecular weight of 23500 (plus or minus 1500) Da, and are positive for Coomassie staining and PAS staining. The protein is a new ligand of receptor-type tyrosine kinases, and can be prepared by standard recombinant techniques.
   Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New ligand for kilo:dalton(s)
                                       18-OCT-1996
                                                                                                         AAR94656 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-388601/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor-type tyrosine kinase; ligand; coomassie staining; PAS staining;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRCTIKKENTPLLNCAKPDODIKFTIKFOEFSPNLWGLEFQKNKDYYIISTSNGSLEGLD
                                                                                                                                                                                                                                                                                                                                      STDGNSAGHSGNNILGSEVALFAGIASGCIFIVIIITLVVLLLXYRRHRKHSPQHTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               SLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD 206
                                                                                                                                                                                                                               DGPPQSPPNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRCEAPPAPULLITCDRPDLDLRFTIKFQEYSPULWGHEFRSHHDYYIIATSDGTREGLE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEPTYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQA 61
                                                                                                                                                                                               EMPPOSPANIYYKV
                                                                                                                                                                                                                                                                      LSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQ
                                                                                                                                                                                                                                                                                                    GSFGRGGSLGLGGGGGMGPREABPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQ
                                                                                                                                                                                                                                                                                                                                                                         PTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP
                                                                                                                                                                                                                                                                                                                                                                                                             NQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTTSPFVKPNPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Page 44; 51pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
   receptor type tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 AA;
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                                       (first entry)
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94JP-0253848.
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                                                                                                          Protein;
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                                                                                                            308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 619.5; DB 17;
Pred. No. 1.2e-42;
8; Mismatches 121;
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       (NH)
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       (mature
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308; 13;

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121

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RESULT 23
AAY71438
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A ligand polypeptide which binds to the extracellular part of a specific receptor-type tyrosine kinase and induces phosphorylation of tyrosine within the cell can be used in the study of the differentiation of blood cells such as the haematopoietic stem cells; of disease processes such as leukaemia, and of the biology of bone marrow transplantation. The ligand plays a role in the differentiation process and the specific ligand target is expressed in undifferentiated blood cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1994;
07-OCT-1994;
26-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligand peptide binding to receptor-type tyrosine kinase - enhance intracellular tyrosine phosphorylation, useful for investigation undifferentiated blood cell behaviour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-209809/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor type tyrosine kinase; TK; ligand; differentiation; haematopoietic stem cell; tyrosine; bone marrow; leukaemia.
                                                                                                                               295
                                                                                                                                                                     327
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                                                                                                                                                                                                                                                                                                                                                                                                                         SLOGGVCLTRGMKVLLRVGO--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD 206
                                                                                                                           EMPPOSPANIYYKV 308
                                                                                                                                                                   DGPPQSPPNIYYKV
                                                                                                                                                                                                              LSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQ
                                                                                                                                                                                                                                                 GSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVO 326
                                                                                                                                                                                                                                                                                            STDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLLKYRRRHRKHSPQHTTT
                                                                                                                                                                                                                                                                                                                                       PTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP 266
                                                                                                                                                                                                                                                                                                                                                                                 NOEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTTSPFVKPNPGS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 162-163; 193pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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94JP-0244433.
94JP-0262882.
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Pred. No. 1.2e-42;
8; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
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뮍 Ś Ŗ, Ś В δ B S 밁 S 밁 δ

AAY71438

standard;

peptide;

89

Query Match
Best Local Similarity
Matches 87; Conserv

Conservative

26.6%;

Score 492; DB 21; Pred. No. 7.5e-33; 1; Mismatches 1;

Length 89; Indels

0

Gaps

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The patent discloses a complex comprising of a B class ephrin and PDZ domain containing protein. B class ephrins function as ligands for Eph receptor tyrosine kinases (RTK) and possess a transmembrane element and a highly conserved cytoplasmic tail at the C-terminus, that contains a PDZ binding site. This complex is used in methods to modulate the interaction of a B class ephrin and PDZ domain containing protein and to identify modulator compounds. It is also used for modulating cellular processes like, axonogenesis, nerve cell interactions and regeneration of nerve cells. The complex is also useful for treating proliferative or differentiative disorders associated with this protein complex. The present sequence is the human ephrin B C-terminal cytoplasmic domain, comprising conserved sequences reminiscent of known or predicted binding sites for PDZ domains. Ephrin B3 is also known as NIERK-2, EIK-13, EFL-6, EIF-3 and LERK-8.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated complex for treating proliferative or differentiative disorders comprises B class ephrin and PDZ domain containing p
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production of homogenous forms of clustered ligands is broadly applicable to improve the affinity and/or increase the activity of a ligand as compared to the native form of the ligand. Ephrin fusion proteins have been constructed, which may be useful for treating neurological disorders. The ephrin fusion proteins are preferably capable of binding to Elk receptor and are especially Efl-6 antagonists. The fusion proteins were constructed after it was demonstrated that similar improved activities could be achieved using Tie-2 receptor ligands. Angiopoletin-1 (Ang-1) is a Tie-2 receptor ligand and is an agonist for Tie-2, whereas angiopoletin-2 (Ang-2) is a naturally occuring antagonist of the Tie-2 receptor. The fibrinogen domains (FD) of Ang-1 and Ang-2 are the receptor-binding domains and dimerized versions, of e.g. Ang-1-FD-Fc
                                                                                                                                                                                                                              Polynucleotide encoding a fusion polypeptide, useful for promoting differential function and influencing phenotype, comprises two subunits containing at least one copy of the receptor binding domain of a ligand
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                                                                 _Bridging_peptide
                                        ELK-L_Ectodomain_2
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Pred. No. 1.2e-28;
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                                                                                                                           Ectodomain
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RESULT 26
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                                                                                                                                                                                                                                                                                                                                  CC to improve the affinity and/or increase the activity of a ligand as compared to the native form of the ligand. Ephrin fusion proteins have been constructed, which may be useful for treating neurological CC disorders. The ephrin fusion proteins are preferably capable of binding to El Rivertine after it was demonstrated that similar improved activities could be achieved using Tie-2 receptor ligands. Angiopoietin-1 (Ang-1) is a Tie-2 receptor ligand and is an agonist for CC activities could be achieved using Tie-2 receptor ligands. Angiopoietin-1 (Ang-1) is a Tie-2 receptor ligand and is an agonist for CC fie-2, whereas angiopoietin-2 (Ang-2) is a naturally occurring antagonist cof the Tie-2 receptor. The fibringen domains (PD) of Ang-1 and Ang-2 are the receptor binding domains and dimerized versions, of e.g. Ang-1-PD-FC (Ang-1 fibringen domain fused to an Fc domain), can bind to the Tie-2 receptor with much higher affinity than monomeric Ang-1-FD (dimerization occurs between the Fc components of adjacent molecules). However, creeptor on endothelial cells unless it is further clustered with goat anti-human Fc antibodies. The novel fusion proteins, mutant versions of Ang-1-FD and Ang-2-FD, were designed that were intrinsically more highly CC clustered. Tie-2 agonist fusion proteins may be used to collegnose or treat, e.g. myeloproliferative or other proliferative and lighterials of and lenkemias.
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Best Local
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                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding a fusion polypeptide, useful for promoting differential function and influencing phenotype, comprises two subunits containing at least one copy of the receptor binding domain of a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12; Fig 14A-E; 97pp; English
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                                                                                                                                                                                                                          GLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGG 86
                                                 DSDGKHETVNQEEKSGP----
                                                                         DPTSNATSRGAEGPLPPPSMPAVAGAAGG
                                                                                                GLENREGGVCRTRIMKIIMKVGODPNAVTPEQLTTSRPSKEADNTVKMATQAPGSRGSLG 414
                                                                                                                        GLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE-PGKENLPG 205
                                                                                                                                                                        AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTRE 146
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92; Conserv
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                                                                                                                                                                                                                                            24.5%; 5c.
44.0%; Pred
32;
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Pred. No. 1.9
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1.5e-28;
1es 72;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 48-49; 55pp; English
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171
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                                                                                                                                                                                                                                                                                                                                                                                                        14 GALLLIGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                         DYYIIATSDGTREGLESLQGGYCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA
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                                                        HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRR
                                                                                                                                                                                                                                                                                                                                                GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                DYYLLSTSNGSLEGIDNQEGGVCQTRAMKILMKVGQD-----
                                                                                                                                                                                                                                GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100;
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- ASSAGSARNHGPTRRPELE - -
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      134
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      DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                                                                                                            GVIMVICRTAISKSIVIEPIYWNSSNSKFIPGQGLVIYPQIGDKIDIICPKV---DSKTV 70
                                                                   GOYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                         PNYBPYKLYLVGGAQGRRÇEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Page 51-52; 55pp; English.
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                                                                                                                                                                                                                                                                                                                  23.9%; Score 443; DB 23; 35.6%; Pred. No. 2.4e-28; tive 36; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liau
                                                                                                                                                                                                                                                                                                                                                                                  Length 229;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                            62;
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122

NQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTTSPFVKPNPGS

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AAWO6333

ID AAWO6333

ID AAWO6633

ID AAWO66XX

II JOANO6

XX IIGAN

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XX Recep

XX Homo

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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW06333 and AAW06334 represent receptor-type tyrosine kinase receptor binding ligands of the invention. These sequences both have the N-terminal sequence represented by AAW06332. The ligands of the invention recognise the fragment of the receptor type kinase receptor represented by AAW06330 (see AAW06331 for full length sequence). The proteins of the invention have a molecular weight of 23500 (plus or minus 1500) Da, and are positive for Coomassie staining and PAS staining. The protein is a new ligand of receptor-type tyrosine kinases, and can be prepared by standard recombinant techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor-type tyrosine kinase; ligand; coomassie staining; PAS staining;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1994;
19-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligand #1 for receptor-type tyrosine kinase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06333 standard; protein; 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New ligand for receptor type tyrosine kinase - has mol.wt. 22
kilo:dalton(s) and is positive for Coomassie and PAS staining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-388601/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASAH ) ASAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131
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            150
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DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVA
      SLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD
                                                                                                         RRCEAPPAFNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE
                                                                                                                                                                         LEPTYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQA 61
                                                                                                                                                                                                                                  LEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREA
                                                               DRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEGLD 121
                                                                                                                                                                                                                                                                                           1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 43; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                              195 AA;
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94JP-0275411.
94JP-0253848.
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                                                                                                                                                                                                                                                                                                                       23.3%;
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                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                           Score 431.5; DB 17;
Pred. No. 1.7e-27;
2; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226
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                                                                                                                                                                                                                                                                                                                                                           195;
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                                                                                                                                                                                                                                                                                                 Gaps
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PTSNATSRGAEG

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RESULT 29
AAW11307
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Best Local
                                                                                                                                                                                                                                                                                                                                                         AAW11307 and AAW11308 represent receptor-type tyrosine kinases. These sequences can be included in the LPM medium of the invention. The medium is used to culture cells capable of producing a ligand for receptor-type tyrosine kinase. The ligand serves as a physiologically active substance to induce enzyme activity and autophosphorylation of tyrosine kinase, which is involved in the development and differentiation of animal and insect cells. The ligand can also be used as in a pharmaceutical preparation for promoting growth of undifferentiated cells. The medium may also include an inducer, such as insulin, an install the medium may also include an inducer, such as insulin, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor-type tyrosine kinase; LPM medium; ligand; autophosphorylation; insect cell; animal cell; growth promoter; undifferentiated cell; insulin; interleukin; fibroblast growth factor; hepatocyte growth factor; nerve growth factor; inducer.
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW11307 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 38-39; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPM cell culture medium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-014848/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor-type tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-1997
                                                                                                                                                                                                                                                                                                                                               interleukin, a fibroblast growth factor, or interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor-type tyrosine kinase ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASAH ) ASAHI KASEI KOGYO KK
 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
                               207
                                                             122
                                                                                          150
                                                                                                                         9
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                                                                                                                                                                                                                    30 LEPVYWNSANKREQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQG 89
                                                                                                                                                                                      σı
                                                                                                                      DRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEGLD
 ST-DGNSAGHSG 192
                               PTSNATSRGAEG 218
                                                                                          SLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD 206
                                                                                                                                                        RRCEAPPAPULLITCORPOLDLRFTIKFQEYSPULWGHEFRSHHDYYIIATSDGTREGLE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ST-DGNSAGHSG 192
                                                             NQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTTSPFVKPNPGS
                                                                                                                                                                                      LEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQA
                                                                                                                                                                                                                                                   1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                 195 AA;
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 195
                                                                                                                                                                                                                                                               23.3%;
45.3%;

    for culturing

                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                   Score 431.5; DB 18;
Pred. No. 1.7e-27;
2; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells which produce
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                  Length 195;
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                                                                                                                         121
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RESULT 30
AAM37671
ID AAM37671
XX AAM37
AC AAM37
XX Pepti
XX Pepti
XX Probe
KW Probe
KW Genet
XX WO200
XX O4-FI
PR 26-FI
PR 27-SI
PR 27-SI
PR 30-JI
XX O4-FI
PR 30-JI
XX WO1-JI
XX WO
                                                                                                                                                                                                                     RESULT 31
ABG46524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP: see ARI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placents. The probes are useful for antenatal diagnosis of
Human; single exon probe; asthma; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID No 37940; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM37671;
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                                            Human peptide encoded by genome-derived single exon probe
                                                                                                                                                                                                ABG46524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #11708 encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-CCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                  102 LTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYI 137
                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                             42 FQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYBFYKLYLVGGAQGRRCEAPPAPNLL 101
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                                                                                                                                                                                                                                                                                                                                                                                                                      FLSGKGLVIYPKIGDKLDIICPRABAGRP----YBYYKLYLVRPEQAAACSTVLDPNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                              standard; Peptide; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 AA;
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2000US-0632366.
2000US-0234687.
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2000GB-0024263
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                                                                                                (first entry
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Pred. No. 7.4
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  cancer; COPD; ILD
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1es 24;
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CC The invention relates to a spatially-addressable set of single exon concluded aridy probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of complements or the 12387 open reading frames derived from the 1264 probes, the notel set of probes which hybridise at high stringency to a collectic acid expressed in the human lung; measuring gene expression in a complement of expressed in the human lung; measuring gene expression in a concluded are a microarray comprising the novel set of probes, the novel set of probes which hybridise at high stringency to a collection of detectably labeled nucleic acids derived from human lung; measuring gene expression in a concluded acid expression in a concluded acid expression of feetectably labeled nucleic acids derived from human lung measuring (a) contracting the array with cof the entray; identifying exons in a eukaryotic genome, comprising cof the entrayet, and (b) measuring the label detectably bound to each grobe of the entrayet, and (b) detecting specific hybridisation of detectably cof the entrayet, and (b) detecting specific hybridisation of detectably comprising exons from genomic sequences of the expression of the exons in the predicted exon, the probe is included comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising one to a single exon probe with the exon, where a common pattern of the exons should be assigned to a single exon, the probes are used for gene that the transmitted of the exons in a serie that the transmitted probable comprising one conditions the probable of the exons in series that the probable of the exons in series and the probable of the exons of the exons in the probable of the e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicoytosis; lymphangicleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis, fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
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03-AUG-2000;
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; 2000US-236359P.
; 2000GB-0024263.
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2000US-0608408.
2000US-0632366.
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230 GAAGGLA--

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--MCWRRRRAKPSESRHPGP 266

Query Match Best Local : Matches

Similarity

11.1%; 37.7%;

Conservative

13;

Score 205.5; Pred. No. 3.5e 13; Mismatches

5e-09

Indels

Gaps

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22;

Length

136; 39;

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           such probe. The probes are useful for producing a microarray for producting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                           Probe; microarray;
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Sequence
                                                                                     Claim 27; SEQ ID No 37803; 654pp;
                                                                                                       analyzing
                                                                                                                                                       Penn
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27-SEP-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                             Peptide #11571 encoded by probe
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                                                                                                                                    2001-488897/53
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                                                                                                      genome-derived single exon nucleic ac: zing gene expression in human placenta
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52; Conservative
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2000US-0608408.
2000US-06323687.
2000US-0234687.
2000US-0236359.
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 mucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a conlection of detectably labeled nucleic acids derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) indicating sequences of the eukaryote; and (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis, neurofibromatosis; familial idiopathic pulmonary disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human peptide encoded by genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-114183/15
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2000US-0632366.
2000US-234687P.
2000US-236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, CC having a fragment identical to the predicted exon, the probe is included comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (b) measuring the expression of each of the exons in several crisquest and/or cell types using hybridisation to a single exon comprising one compression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, a peptide comprising one compression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (CODD), interstitial lung disease (ILD), familial idiopathic pulmonary (CC haemosiderosis, pulmonary disease, tuberous sclerosis, Gaucher's disease, lung cancer, chronic obstructive pulmonary disease, CC (CODD), interstitial lung disease (ILD), familial idiopathic pulmonary (CC haemosiderosis, pulmonary histiocytosis, lymphangiolejomyomtosis, pulmonary disease, sarcoidosis, pulmonary histiocytosis, lymphangiolejomyomtosis, pulmonary disease, The present sequence is a peptide/protein encoded by a single exon probe of the invention.

CC of the sequence data for this patent did not form part of the protein data for this patent did not form part.
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                            axonogenesis; an differentiative
                                                                                                                                                                                                                                                                                                             Human ephrin B2 C-terminal cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                 Modified-site
                                                                  Modified-site
                                                                                                   Modified-site
                                                                                                                                       Region
                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                           cellular process; nerve cell
                                                                                                                                                                                                                                                                              PDZ domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                   standard; peptide; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 AA;
                                                                                                                                                                                                                                                           B class ephrin; Eph receptor tyrosine kinase; RTK; modulator; ocess; nerve cell interaction; regeneration of nerve cell;
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                                                                                                                                                                                                                      antiproliferative; proliferative disorder; treatment;
ve disorder; human; cytoplasmic domain.
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71..75
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                                                                                                                                       Location/Qualifiers 50..68
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37.7%;
              "Conserved
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Pred. No. 3.
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              tyrosine phosphorylation site"
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                                                                                     site"
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses a complex comprising of a B class ephrin and PDZ domain containing protein. B class ephrins function as ligands for Eph receptor tyrosine kinases (RTK) and possess a transmembrane element and a highly conserved cytoplasmic tail at the C-terminus, that contains a PDZ binding site. This complex is used in methods to modulate the interaction of a B class ephrin and PDZ domain containing protein and to identify modulator compounds. It is also used for modulating cellular processes like, axonogenesis, nerve cell interactions and regeneration of nerve cells. The complex is also useful for treating proliferative or differentiative disorders associated with this protein complex. The present sequence is the human ephrin BZ C-terminal cytoplasmic domain, comprising conserved sequences reminiscent of known or predicted binding sites for PDZ domains. Ephrin B2 is also known as Htk-L, ELF-2, LERK-5 and NLERK-1.
detection; diagnosis; identification; cytostatic; neuroprotective;
nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
antiinflammatory; cardiant; gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated complex for disorders comprises E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-2000
                                                                                                                        Human pancreatic cancer antigen protein sequence
                                                                                                                                                                            09-MAR-2001
                                                                                                                                                                                                                                                                             AAB54187 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 1; 59pp; English.
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                                                                            pancreas;
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79
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                                                                            pancreatic cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 204; DB 21;
Pred. No. 2.5e-09;
4; Mismatches 11
                                                                                                                                                                                                                                                                                B
                                                                            pancreatic cancer antigen;
                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                 AAY71436;
                                                                                                                             AAY71436 standard;
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-TTENNYCPHYEKVSGDYGHPVXIVQEMPPQSPANIYYKV 106

peptide;

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consists and antigen particular can be used to partering cancer antigens can be used to partering the state of prevent and antiinflammatory activities, and can be used for conditions can be identified and proteins can be used for conditions can be identified. The parterest cancer antigens can be used to condition or a susceptibility to one in a condition can be identified. The parcreatic cancer antigens can be used to design nucleic conditions and antigens can be screened for. The parcreatic cancer antigens can be screened for. The conditions can be used to design nucleic conditions and antigens can be used to design nucleic conditions of conditions can be used to design nucleic conditions of conditions can be used to generate antibodies can diagnostic methods. The proteins can be used to generate antibodies conditions can be used to partity, detect and target the polypeptides, including conditions can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or conditions and in the conditions of the conditions can be used to design and antigens can be used to generate antibodies conditions can be used to treat or prevent neural, immune system, muscular, reproductive, disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1078; 1379pp; English.
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                                                                                235 LALLILIGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEP 290
LTVLLLKL----
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ll; Mismatches
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Human

ephrin

B1 C-terminal cytoplasmic domain

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                                                                                                                                                The patent discloses a complex comprising of a B class ephrin and PDZ domain containing protein. B class ephrins function as ligands for Eph receptor tyrosine kinases (RTK) and possess a transmembrane element and a highly conserved cytoplasmic tail at the C-terminus, that contains a PDZ binding site. This complex is used in methods to modulate the interaction of a B class ephrin and PDZ domain containing protein and to identify modulator compounds. It is also used for modulating cellular processes like, axonogenesis, nerve cell interactions and regeneration of nerve cells. The complex is also useful for treating proliferative or differentiative disorders associated with this protein complex. The present sequence is the human ephrin B1 C-terminal cytoplasmic domain, comprising conserved sequences reminiscent of known or predicted binding sites for PDZ domains. Ephrin B1 is also known as LERK-2, Elk-L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDZ domain; B class ephrin; Eph receptor tyrosine kinase; RTK; modulator; cellular process; nerve cell interaction; regeneration of nerve cell; axonogenesis; antiproliferative; proliferative disorder; treatment; differentiative disorder; human; cytoplasmic domain.
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Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITG-ABLIGI), expressed DNA sequences (ABLIGITG-ABLIGIS), expressed DNA sequences (ABLIGITG-ABLIGIS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic a
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11-JUL-2000;
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DB; ABL02724.
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Pred. No. 1.9e-06;
O; Mismatches 136;
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genes from Drosophila and
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  33 VYWNSANKRFQAEG-GYVLYPQIG---
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                                                             Aldrich TH,
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94US-0299567.
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Matches 64
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03-DEC-1993;
09-MAY-1994;
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                            WPI; 1995-106811/14.
N-PSDB; AAQ85887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig
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                                                                                                            Cerretti
                                                                                                                                                                                                                93US-0109745.
93US-0114426.
93US-0161132.
94US-0240124.
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                                                                                                                                                                                                                                                                                                                                                      94WO-US09282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----MERDRGAAHSLE-----PGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine kinase receptor; tumorigenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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RESULT 41
AAW02567
ID AAW02
XX AAW02
XX Lerk-
XX Lerk-
XX Lerk-
XX Lerk-
XX Ineuro
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                         WPI; 1996-287171/29.
N-PSDB; AAT32700.
                                                                                                                                                                                                                                                           01-MAR-1995;
06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW02587 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hek proteins, to purify hek proteins, and to carry diagnostic of cytotoxic agents to particular leukaemia cells that express the antigen. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lerk-6; hek; elk; cell surface receptor; culture; reagent;
neuron; disorder; injury; delivery agent; diagnostic; ther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lerk-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW02587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                             05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9617925-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lerk-7; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 36; 45pp; English.
                                                                                                                                                                                                       (IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   also AAR71482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKPVSEMP-----PGKENLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL----DLRFTIKF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPG------GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGVGPGAGPGPGGGAEQYVĽYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                           95US-0396946.
94US-0351025.
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                                                                                                                                                                                                                                                                                                                                                95WO-US15781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.7%;
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Pred. No. le-06;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223
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12;

isolated human Lerk-7 cytokine -

which binds

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cell

surface

7;

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RESULT 42
AAR91283
ID AAR91
XX AAR91
XX LERK-
XW LERK-
XW INCLERK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a murine cytokine, Lerk-6, encoded by ART32700. A fragment of murine Lerk-6 DNA was isolated by PCR for use a probe for a human Lerk-6 homologue. The probe however led to the identification of a human Lerk-7 gene (see ART32699). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptors elk, hek for treating neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                               WPI; 1996-209575/21.
N-PSDB; AAT14009.
                                                                                                                                                                                                                                                                                                              03-OCT-1995;
05-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LERK-6; hek; elk; cell surface receptors; culture; reagent;
neurons; disorder; injury; delivery agent; diagnostic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR91283 standard;
                      screening procedures
                                               Isolated DNA encoding cytokine designated LERK-6 which binds to and elk cell surface receptors - useful for drug delivery and
                                                                                                                                                                                                          Cerretti
                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9610911-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LERK-6 protein
                                                                                                                                                                                                                                                               AWWI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDP----TSNATSRGAEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
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Pred. No. 1.3e-06;
9; Mismatches 69;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The LERK-6 polypeptide encoded can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by
                                                                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                                                                     LERK-6 polypeptide; hek receptor; elk receptor; human; murine; cell proliferation; neural growth; neural tissue; neurological neurodegenerative; excitotoxicity.
The invention relates murine and human LERK-6 polypeptides that bind hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombing production of the proteins. LERK-6 polypeptides may be useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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contact with the polypeptide.
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                                                                                                             WPI; 1999-243567/20
N-PSDB; AAX32761.
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                                                              Claim
                                                                                    New cytokine designated LERK-6
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Pred. No. 1.3e
L9; Mismatches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enhancement, stimulation, proliferation or growth of cells expressing hek or elk receptor. The ligand and receptor complex may be involved ineural growth, development and/or maintenance. LERK-6 can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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L.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RASULT 45
AAW71076
ID 7006
ID 7007
XX AAW71
AC AAW71
XX 20-0C
XX Amino
XX Mouse
KW Mouse
KW Molse
KW B61;
KW Lincre
KW B1;
KW Alzee
KW B00ne
XX Mus 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis and treatment of disorders associated with the Elf-1 gene, e.g.
   Modified-site
                                                                                                     Mus sp.
                                                                                                                                              Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand B61; LERK-2; proliferation; differentiation; intracellular signaling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;
                                                                                                                                                                                                                       Amino acid sequence of a mammalian Elf-1 protein.
                                                                                                                                                                                                                                                     20-OCT-1998
                                                                                                                                                                                                                                                                                 AAW71006;
                                                                                                                                                                                                                                                                                                             AAW71006 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel mouse EPH receptor ligand, Elf-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 86; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheng H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-1995;
19-SEP-1994;
                                                         Peptide
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                                                                                                                                 formation.
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                                                                                                                                                                                                                                                                                                                                                                                   EAPEPIFTSNSSCSGLGG
                                                                                                                                                                                                                                                                                                                                                                                                               GDP----TSNATSRGAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1996-188446/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT
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78
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ilarity 29.3%;
Conservative 1
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94US-0308814.
 /note= "mature protein"
38
                               /note= "signal peptide"
21..209
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 176; DB 17;
Pred. No. 1.5e-06;
9; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AAR94766), is involved
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19-SEP-1994;
27-FEB-1995;
                                                                                                                                                                                                                                                                                                                           The present sequence represents a mammalian EPH receptor ligand designated Blf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended forcessing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding Elf-1 protein that binds to EPH-type - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                       Sequence
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175
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)B; AAV42926.
EAPEPIFTSNSSCSGLGG
                            GDP----TSNATSRGAEG 218
                                                      ----PNLVDRPCLR--LKVYVR-
                                                                                  REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP
                                                                                                             GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP--
                                                                                                                                       QGRRCEAPPAPULLLTCDRPDL---DLRFTIKFQEYSPULWGHEFRSHHDYYIIATSDGT
                                                                                                                                                                       VYMNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
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                                                                                                                                                                                                                              58;
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                                                                                                                                                                                                                                                                                       209 AA;
                                                                                                                                                                                                                              Conservative
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94US-0308814.
95US-0393462.
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                                                                                                                                                                                                                                            9.5%;
29.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "potential N-linked glycosylation
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                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                            Score 176; DB 19;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosylation
                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                           209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor
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RESULT 46 AAY06822

09-MAR-2001

(first entry)

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RESULT 47
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                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LERK-6 polypeptide; hek receptor; elk receptor; human; murine; cell proliferation; neural growth; neural tissue; neurological neurodegenerative; excitotoxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-243567/20
N-PSDB; AAX32767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 42; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cytokine designated LERK-6
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                                       AAB54058;
                                                                   AAB54058
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                     VYWNSANKRFOA----EGGYVLYPOIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                              GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISAT
                                                                                                                                                                           QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS
                                                                                                                                                                                                           VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-
                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                     Similarity
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                                                                   standard;
                                                                                                                                                                                                                                                                                                                                   213
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                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US17772
                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry
                                                                                                                                                                                                                                                                    9.5%; Score 175.5; DB 20
36.8%; Pred. No. 1.7e-06;
tive 14; Mismatches 51;
                                                                     218
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disease;
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gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

Agonists and antagonists to the antigens can be used for. The pancreatic cancer antigens can be used to generate cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including proteins can be used to purify detect and target the polypeptides. The proteins can be used to generate antibodies of the proteins can be used to generate antibodies and proteins can be used to generate antibodies. The proteins can be used to generate antibodies of the proteins can be used to generate antibodies. The proteins can be used to generate antibodies. The proteins can be used to generate antibodies of the proteins can be used to generate antibodies. The proteins can deal to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proteins can deal to the proteins can be used to generate and the proteins can be used to generate antibodies.
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Best Local S
Matches 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-579444/54.
N-PSDB; AAC98823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences used in the exemplification of the present
120 YSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
                                                                                                                                              67
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                                                                                                                                         YE---DHŚVADAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQR 123
                                                                                                                                                                                                                                    ARPPGPHSSPN--YEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                PGGVRVGALLLLGVLGLVSGLSL---EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR 64
                                                                                                                                                                                                                                                                                                                                          PGQARAMEFLWAPLIGICCSIAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assays for diagnosing a pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 172.5; DB 2
Pred. No. 3.1e-06;
0; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
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AAR94767
ID AAR94
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                                                                                                                                                          Matches
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diagnosis;
                                                                                                                                                                                                                                                                                                                                      A novel chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAT15009) obtd. from an embryo cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis and treatment of disorders associated with the Elf-1 gene, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicken
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                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 88-89; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dementia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-1995;
19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1995;
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                                                                                                                                                                                                                                                                                                                     pathways mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 FTPFTLGKEFKEGHSYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHDNPQE 176
                                                                                                           5
                                                                                                                                                                                       Local Similarity
                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1996-188446/19.
RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPHLLLTCDRPDL---DLRFTIKFQEYSP 122
                                                  AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVEVSINDYLDIYCPHY 64
                                                                                                        ALLULGVLGLVSGLSLEP------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ή
                                                                                                                                                             49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor ligand; dementia; tachycardia; transgenic animal.
                                                                                                                                                                                                                                                                   200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor ligand Elf-1.
                                                                                                                                                             Conservative
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94US-0308814.
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33..157
/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Mat_protein
                                                                                                                                                                                       9.3°;
35.3°;
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                                                                                                                                                                                                                                                                                                                   the EPH-type receptor.
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                                                                                                                                                             16;
                                                                                                                                                                                       Score 172; DB 1
Pred. No. 3e-06;
                                                                                                                                                                Mismatches
                                                                                                                                                                                                             DB 17;
                                                                                                                                                                                                                Length 200;
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RESULT 49
AAW71007
Query Match
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Matches 49
                                                                                         The present sequence represents an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended to transplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-1995;
19-SEP-1994;
27-FEB-1995;
                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW71007;
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                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV42927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      artificial liver; cartilage; bone formation
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                                                                                                                                                                                                                                                                                             Claim 1; Columns 75-78; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng H,
                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                              1998-466665/40.
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l Similarity
49; Conserv
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95US-0393462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 61..150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "contains a Cys4"
              35.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an avian
  16;
                Score 172; DB 1
Pred. No. 3e-06;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elf-1 protein
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                            19;
     58;
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                             Length 200;
    Indels
     16;
     Gaps
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Query Match Best Local S Matches 66

l Similarity 66; Conserv

Conservative

9.2*;

Score 169.5; DB 1 Pred. No. 4.9e-06; 8; Mismatches 82

82; 16;

Indels Length

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Sequence

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RESULT 50
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ID AAR71
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                                                                                                                                                                                                                                                                                                        20-AUG-1993;
30-AUG-1993;
03-DEC-1993;
09-MAY-1994;
                               The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antign. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                          New isolated DNA encoding hek-L protein or its fusion useful as assay reagent or for carrying therapeutic andiagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human hek-L
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                                                                                                                                                                                                                                                                                                                                                                   17-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligand; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR71482;
                                                                                                                                                                                                                                                           Beckmann MP,
                                                                                                                                                                                                                                                                                                                                                                                                                WO9506065-A
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                                                                                                                                                                                                                        1995-106811/14.
DB; AAQ85888.
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                         AAR71481.
                                                                                                                                                      Page 38; 45pp; English.
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93US-0114426.
93US-0161132.
94US-0240124.
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23..201
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Search completed: February 11, 2003, 12:03:00 Job time : 32.2264 secs

Title: Perfect score:

US-10-021-121-4 1850

Scoring

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Minimum DB Maximum DB

seq length: 0
seq length: 2000000000

Post-processing: Minimum Match Maximum Match

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protein

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Total number of hits satisfying chosen parameters:
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US-08-28-077-240-2
US-08-28-054-4
US-08-29-567-6
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APPLICANT: Holland, Sacha

APPLICANT: Hobamalu, Geraldine

APPLICANT: Mbamalu, Geraldine

APPLICANT: Mbamalu, Geraldine

TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED

TITLE OF INVENTION: TYROSINE KINASES

TITLE OF INVENTION: TYROSINE KINASES

FILE REFERENCE: 11757.23USWO

CURRENT FILING DATE: 1999-03-12

CURRENT FILING DATE: 1999-03-12

EARLIER FILING DATE: 1997-07-04

EARLIER FILING DATE: 1997-07-04

EARLIER FILING DATE: 1996-07-05

NUMBER OF SEG ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEG ID NO 3

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US-09-214-631-3
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GENERAL INFORMATION
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 339; Conserv
                                                                                                                                                                                                                                                                   LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
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                        VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
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PCT-US95-501-2
US-08-455-001-2
US-08-920-440B-10
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US-09-173-492-10
US-09-173-133-10
US-09-173-133-10
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US-08-455-001-4
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Pred. No. 1.1e-146;
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US-08-436-044-2
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Best Local Similarity
Matches 139; Conserv
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Patent No. 5624899
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Matthews, William
TITLE OF INVENTION: HTK LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genencech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/436,044 FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                       DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                   GOYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
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GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253
                                  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC 250
                                                                        DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193
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460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                   34.5%; Score 637.5; DB 1;
42.1%; Pred. No. 1e-45;
Live 49; Mismatches 129;
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US-08-436-054-2
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Patent No. 5864020
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Matthews, William
TITLE OF INVENTION: HTK LIGAND
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 139; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,054
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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251
                                                                       191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC
                                                                                                                                                        134 DYYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP:
                                                                                                                                                                                              74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                         17 GILMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                                                                                                                                                                                                                                          14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                               PNYEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGGREAEPGELGIALRGGGAADPPFCPH 310
                                       GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
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  WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                  DYYTISTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193
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T: 460 Point San Bruno Blvd
South San Francisco
California
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42.1%; Pred. No. 1e-45;
tive 49; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9508812
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: 5.25 inch, 360 Kb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
TOPOLOGY: line-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                     WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                  DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193
                                                                                                                                                                                                                           GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                             PNYEFYKLYLVGGAQGRRCEAPPAPNILLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                         GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253
                                                                                                            GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                    DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGO--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV----DSKTV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                            34.5%; Score 637.5; DB 5;
42.1%; Pred. No. 1e-45;
rative 49; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTK LIGAND
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 336;
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; MOLECULE TYPE: protein US-08-213-403-2
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,693

PILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 373-0644
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US-08-213-403-2
                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.2%; Score 632; DB 1; Length 346; Best Local Similarity 39.5%; Pred. No. 3e-45; Matches 145; Conservative 48; Mismatches 116; Indels
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
TOPOLOGY: line
WOLFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/213,403
FILING DATE: 15-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5512457el Cytokine Designated elk Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZLECOPHICE: (200)
TELEPHONE: (206) 7
232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ----
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STATE: Washington
                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                       64 CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
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                                                                                                                                                                                                                                                                                                 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVTYPKIGDKLDII
                                                                                                                                                                                                                                                                                                                                    PGGVRVGALILLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                        SRPSKEADNTVKWATQAPGSRGSLGDSDGKHETVNQEEKSGP-----
                                                                                                          SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                                                                                                                                   PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGWKVLLRVGQSPRGGAVPRKPV 181
                                                                                                                                                                                                                                                           CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                Indels 58;
                                                                            -GASGGSSGDPD 231
    ----RAAALSL
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                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-458-077-2
                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

APPLICANT: Beckmann, M. Patricia

APPLICANT: Baum, Peter R

APPLICANT: Carpenter, Melissa

TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand

NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07,
FILING DATE: 13-NOV-1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
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                                                                                                                                                                                        8 PGGVRVGALILLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                            CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
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    PNYMGLERKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                    PNIWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                                CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                                                      PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
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amino acid
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ilarity 39.5%;
Conservative 48
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                                                                                                                                                                                                                                              Score 632; DB 1
Pred. No. 3e-45;
                                                                                                                                                                                                                                Mismatches 116; Indels
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                                                                                                                                                                                                                                                                DB 1; Length 346;
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                                                                                                                                                  ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-741-2
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Patent No. 5670625
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R
                                                                          Matches
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: MICTOSOFT WORD FOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,741
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
ATTORNAMY/ACTORY
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                                                                                                                                                                                                                                                            TELEFAX: (206) 233-06
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: 346 amino acid
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
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STREET: 5.
TTY: Seattle
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                                      8 PGGVRVGALLILGVLGLVSGL-----SLEPVXWNSANKRFQAEGGYVLYPQIGDRLDLL 61
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    346 amino acids
amino acid
    CY: linear

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ft Word for Apple, Version 5.1a
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                                                                        Score 632; DB 1; Length 346; Pred. No. 3e-45; B; Mismatches 116; Indels
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US-08-747-240-2
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                                                                                                                 FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08747240 Patent No. 5728813
MOLECULE TYPE: protein -08-747-240-2
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APPLICANT: Lyman,
APPLICANT: Beckman
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MEDIUM TYPE: Flopy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 12-NOV-1996
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CORRESPONDENCE ADDRESS:
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TLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand
TOP SEQUENCES: 2
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                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
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Beckmann, M. Patr
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Baum, Peter R
Franter, Melissa
Frong
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                                                                                                                                                  ZIP: 10591-6707

ZIP: 10591-6707

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/299,567

FILING DATE: 01-8EP-1994

CLASSIFICATION + 435

ATTORNEY/AGENT INFORMATION:

NAME: Kempler, Gail M.

REGISTRATION NUMBER: 32,143

REFERENCE/DOCKET NUMBER: REG 290

TELECHNUE: 914-345-7400

TELEPHONE: 914-345-770
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Best Local Similarity 39.5
Matches 145; Conservative
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Patent No. 5747033
                                                                                                                       TELEFAX: 914-34
INFORMATION FOR SEQ
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                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD
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                  TOPOLOGY: un
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STATE: New York
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                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Regeneron Pharmaceuticals, Inc
777 Old Saw Mill River Road
                                                                                                                                          914-345-77
                       unknown
protein
                                                                                                                       ID NO: 6:
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Best Local Similarity
                                                                                                                                                                APPLICATION NUMBER: US/08/436,044
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
                       TELEX:
                                                                                                                                                                                                                                                                                                                   ZIF: 3400
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
TELERA: 410,371-7168
TELEX: 910/371-7168
TELEX: 90 ID NO:
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bennett, Brian D. APPLICANT: Matthews, William TITLE OF INVENTION: HTK LIGAND
     SEQUENCE
                                                                                            REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Genented, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMBER OF SEQUENCES:
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                                       TELEPHONE: 910/-
TELEPHONE: 910/-
1071-7168
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                                                                                                                           NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANIYYKV 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LLILGVAGAGGA-------MCWRRRRAKPSESRHPGPGSFGRGGSLGL
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                                                                              415/225-1994
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                                                                                                                 902D3
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RESULT 11
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Best Local Similarity
Matches 135; Conserv
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                                                                                                                                                  251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GALLLIGVLGIVSGLSLEPVYWNSANKRFQAEGGVVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                        74 PNYEFYKLYLVGGAQGRRCEAPPAPNILLTCDRPDIDIRFTIKFQEYSPNIWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GVLMVLCRTAISKSIVLEÞIÝMNSSNSKFLÞGQGLVLÝÞQÍGDKLDIICÞKV---DSKTV 70
                                                                                                      YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                       YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                                                                                                  KYRRRHRKHSPOHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303
                                                                                                                                                                                                                                                          GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                                                                DYYTTSTSNGSLEGLDNQEGGVCQTRAMKTLMKVGQDASSAGSTRNKDFTRRPELEAGTN 190
                                                                                                                                                                                                                                                                                                                                 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                                                                                         GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQXNK 130
                                                                                                                                                                                   WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                         GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.0%; Score 629.5; DB 1;
40.9%; Pred. No. 4.6e-45;
tive 52; Mismatches 130;
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Sequence 4, Application US/08436054 Patent No. 5864020 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: US/08/
PILING DATE: 05-MAY-1995
CLASSLEICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277
FILING DATE: 20-UUL-1994
ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA: APPLICANT: Bennett, Brian D. APPLICANT: Matthews, William TITLE OF INVENTION: HTK LIGAND NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: STATE: C STREET: 460 Point San Bruno CITY: South San Francisco ADDRESSEE: INFORM California USA amino acids 08/277722 US/08/436,054 902D1 Blvd

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TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-271-948-2
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US-08-271-948-2
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Patent No. 6303769
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
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Best Local (
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                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION HUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2823
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                   TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,948
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cerretti, Douglas P.
APPLICANT: Reddy, Pranhitha
TITLE OF INVENTION: No. 6303769el Cytokine Designated Lerk-5
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 51 Uni
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                                                                                                                                                                                                                                                                                                           ASSIFICATION:
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Y: linear
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51 University Street
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40.9%;
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Pred. No. 4.6e-45;
2; Mismatches 130;
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PCT-US95-08534-2
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GENERAL INFORMATION:
APPLICANT: Immunex Corporation
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                                                                                         TELEX: 756822
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS.
    TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
                                                                                                                                                      NAME: Anderson, Kathryn A.
REGISTRATION NUWBER: 32,172
REFERENCE/DOCKET NUWBER: 2823-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 08-JUL-1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OBERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION NUMBER: PCT/US95/08534
FILING DATE: 06-UUL-1995
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CORRESPONDENCE ADDRESSES: Immunex Corporation
STREET: 51 University Street
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TITLE OF INVENTION: Novel Cytokine Designated Lerk-5
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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PCT-US95-08812-4
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                                                          ; TOPOLOGY: PCT-US95-08812-4
                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
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Best Local Similarity
Matches 135; Conserv
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APPLICANT: Genent
Query Match
Best Local Similarity
Matches 135; Conserv
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MEDIUM TYPE: 5.25 inch, 360 Kb fl
COMPUTER: IBM PC compattible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0881
                                                                                                                                                                                                                                                                               CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                         NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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   Conservative
                                                                         linear
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40.9%; Pred. No. 4.6e-45;
tive 52; Mismatches 130;
 34.0%; Score 629.5; DB 5;
40.9%; Pred. No. 4.6e-45;
tive 52; Mismatches 130;
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      WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
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APPLICANT: Holland, Sacha
APPLICANT: Mommalu, Geraldine
APPLICANT: Mommalu, Geraldine
APPLICANT: Mommalu, Geraldine
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFF
TITLE OF INVENTION: BY TRANSVEMBRANE LIGANDS FOR ELF
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: FOT/CA97/00473
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 333
TYPE: PRT
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Best Local Similarity 40.9%;
Matches 135; Conservative 54
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GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
                                                                                                               GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
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RESULT 17
US-09-214-631-13
US-09-214-631-13
Sequence 13, Application US/09214631
Patent No. 6413730
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
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US-09-214-631-5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-631-5
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APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
                                                                                                                                                                                           339 ANIYYKV 345
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                                                                                                                                                                                                                                                                                       STIASPKGGSGTAGTEPSDIIIPL---FTTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGGRWLGKWLYAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGGVRVG----ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                            -----LLLLGVAGAGGA-------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRPSKEADNTVXMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                                                                                                                                                                                                                 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
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CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 11
SEQ ID NO 11
LENGTH: 82
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US-09-214-631-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 89
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: DY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: 1999-03-12
CURRENT APPLICATION NUMBER: 05/03-12
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSIIE KINASES
FILE REFERENCE: 11757.23USWO
                                              308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 RRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311
                                                                                                                                             252 RRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEPGELGIALRGGGAADPPF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 EKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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                                                                                                                                                                                                Local Similarity es 44; Conserv
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                             CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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113730
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ilarity 47.3%;
Conservative
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                                                                                              RAAALSISTLASPKGGSGTAGTEPSDIIIPLR---TTENNY 49
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                                                                                                                                                                                                Score 201; DB 4; ]
Pred. No. 5.1e-10;
9; Mismatches 24;
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82
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RESULT 19

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LENGTH: 82
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                                                                                                                                                                                                                                                                                                          ZIP: 10591-6707

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994

CLASSIFICATION: 435
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CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1996-07-05
UNMBER OF SEO ID NOS: 13
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APPLICANT: Pawson, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR TITLE OF INVENTION: TYROSINE KINASES FILE REFERENCE: 11757.23USWO
                                                                                 TELBFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Kempler, Gail M.

REGISTRATION NUMBER: 32,143

REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 AEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 SEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 82
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les 38; Conser
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                                        STRANDEDNESS
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New York
                                                              amino acids
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TYPE:
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Pred. No. 5.6e-10;
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                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acid
                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 03-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                                                                              NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 PTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 219
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Local 64;
                                                                                             TELEFAX: 756822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 SSGAGÞGÞGGGAEQÝVLÝMVSRNGYRTCNÁSQGFK-RWECNRÞHAÞHSÞIKÞSEKFQRÝS 126
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                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFSLGYEPHAGHSYYYISTPTHNLH-----WKCLR--WKVFVCCASTSHSG---EKPV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYS 121
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64; Conservative
                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WASHINGTON
                                                                                                                            (206) 587-0430
(206) 233-0644
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28.4%; Pred. No. 1.3e-07;
ive 22; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 234;
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Gaps

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US-08-453-943-2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
110 03-DEC-1993
                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word for Apple, CURRENT APPLICATION NUMBER: US/08/457 ^^ FILING DATE:
                                                                                                                                                                                                                                                                                     FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
AND AUGUST INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOSINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System:
                                                                SEQUENCE CHARACTERISTICS
LENGTH: 238 amino acid
                                                                                                                                                      NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223
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                          TOPOLOGY:
                                           LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKPVSEMP-----PGKENLP 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPG-----GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
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Similarity 28.4%;
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protein
                                                                                                                                                                                                                                                                                                                                                                                                             US 08/114,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Mismatches 80; Indels 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 179; DB 1;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                    APPLICATION NUMBER: US 08/161,132
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/114,426
PILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/109,745
PILING DATE: 30-AUG-1993
PRIOR APPLICATION UNMBER: US 08/109,745
PILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SBESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BECKMANN, M.
APPLICANT: CERRETTI, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: CERRETTI, DOUGLAS P. ITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURPACE ITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
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CLASSIFICATION:
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                                                                                                                                 TELEFAX:
  POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/057,121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG--- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPG-----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN
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                                                                                                                                   (206) 233-0644
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linear
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Pred. No. 1.3e-07;
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US-09-358-734-2
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Best Local Similarity 28.4
Matches 65; Conservative
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APPLICANT: BECKMA
                                                                                                                                              FILING DATE: 20-AUG-1993
ATTORY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                          INFORMATION FOR SEQ ID NO: 2:
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Lent No. 6274117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acid
                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 20-AUG-
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/358,734
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                                 amino acids
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 TYPE:
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                                                                                                                              (206) 233-0644
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MENTION: CYTOKINE THAT BINDS THE CELL SURFACE
MENTION: RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BECKMANN, M. P
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protein
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                                                                                                                                                                                                                                                                                US 08/109,745
                                                                                                                                                                                                                                                                                                                                     US 08/114,426
                                                                                                                                                                                                                                                                                                                                                                                            08/240,124
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                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-299-567-7
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Best Local
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                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                       TELEFAX: 914-345-7721 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                                                                                                                         NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: RE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: //.
STREET: //.
Tarrytown
Tarrytown
York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                       33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--RARPPGPHSSPNYEFYKLYLYGGAQGR 90
                                                                                                             / Match 9.5%; Score 176.5; DB 1; Local Similarity 31.9%; Pred. No. 1.1e-07; ses 43; Conservative 14; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 GPG-----GALG----NRHAVYWNSSNOHLRRE-GYTVQVNVNDYLDIYCPHYN
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
RCEAPPAPULLLTCDRP---DLDLRFTIKFQEYSPULWGHEFRSHHDYYIIATSDGTREG 147
                                     VXWNGSNPKFXRXEGYTIXVXXNDYLDIICPHYEXXXXXXXAGXXXXECYXLYLVXXEXYX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 28.4
65; Conservative
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777 Old Saw Mill River Road
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Pred. No. 1.3e-07;
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RESULT 27
US-08-920-440B-2
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US-09-609-324A-2
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                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08920440B Patent No. 5919905
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Best Local 9
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APPLICANT: Cerret
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CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 08/920,440
PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1994-:
NUMBER OF SEQ ID NOS: 10
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PRIOR APPLICATION NUMBER: 08/318,393
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TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
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ORGANISM: LERK-6
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                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: System 7.6
                                                                                                                                                                                                                                                                    APPLICANT: Cerretti, Douglas P
TITLE OF INVENTION: Cytokine D
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 EAPEPIFTSNSSCSGLGG 167
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                                                                                                       COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
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        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                        Immunex Corporation
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29.3%; Pred. No. 1.7e-07;
ative 19; Mismatches 69
                                                                                                                                                                                                                                                             Cytokine Designated LERK-6
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Best Local Similarity
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cerretti, TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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CITY: Seattle
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51 University Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440B
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTEATION NUMBER: 34,347
127 ----PNLVDRPCLR--LKVYVR-----
                                                      145 REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                               69 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 126
                                                                                                                                                                  88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
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Query Match
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Patent No. 6232447
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                                                                                                                                     TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acid
                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CETTELLANT: CETTETTI, Douglas P.
RITLE OF INVENTION: Cytokine Designated LERK-6
UNDBER OF SEQUENCES: 10
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                                                                                                                                                                                                                    NAME: Henry, Janis C. REGISTRATION NUMBER:
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les 58; Conservative
                                                                    TOPOLOGY:
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FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                   184 amino acids
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                                                                                                                                                     (206)
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 9.5%;
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 Score 176;
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Length 184;
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US-09-165-533-2
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                                                                                                                           Query Match
Best Local Similarity
Matches 58; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cerretti, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
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                                                                                              VYWNSANKRFOAE----GGYVLYPQIGDRLDLLCPRARPFGFHSSPNYEFYKLYLVGGA 87
GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISATP--
                                 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
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                                                                 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 68
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51 University Street
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9; Mismatches 69
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RESULT 32
PCT-US95-15781-2
; Sequence 2, Application PC/TUS9515781
; GENERAL INFORMATION:
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PCT-US95-12779-2
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GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 6
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12779
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
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NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2826-WO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 176; DB 5;
Local Similarity 29.3%; Pred. No. 1.7e-07;
es 58; Conservative 19; Mismatches Conservative 19;
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CITY: Seattle
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51 University Street
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In Release #1.0, Version #1.25
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; Sequence 2, Application US/08455001
; Patent No. 5795734
; GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, an
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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US-08-455-001-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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COMPUTER READABLE FORM:
MEDITY TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2829-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,025
FILING DATE: 06-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cycokine Designated Lerk-7
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                            150 EAPEPIFTSNSSCSGLGG
                                                                                                                                                                                                                                                                                       205 GDP----TSNATSRGAEG 218
                                                                                                                                                                                                                                                                                                                                      127 ----PNLVDRPCLR--LKVYVR
                                                                                                                                                                                                                                                                                                                                                                          145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
APPLICATION NUMBER: US 08/396,946
FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                               69
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CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                           GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISATP-- 126
                                                                                                                                                                                                                                                                                                                                                                        REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
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51 University Street
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Pred. No. 1.7e-07;
                                                                 and
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                                                                 Uses Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 184;
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US-08-308-814-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTMARE: ASCII (text)
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: VITAGE MILLERY
                                                                                                                                                                                                                                                                                              sequence 2, Application US/08308814
satent No. 6268476
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
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             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                 APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands,
TITLE OF INVENTION: Thereto
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                            175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                      STREET:
                                                                                                  COUNTRY:
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60 State Street
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ASCII (txt)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 176; DB 1
29.3%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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PCT-US95-11869-2
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                                                        ; LENGTH: 209 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-11869-2
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
TITLE OF INVENTION: EPH NO.
TITLE OF INVENTION: Thereto
TITLE OF INVENTION: Thereto
TITLE OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TAMBUTER: TEM PC COMPATIBLE
TAMBUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 29.3%;
Matches 58; Conservative 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Applicati
GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                             TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acid
                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/0
FILING DATE: 19-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
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                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                              E: (617)
(617) 22
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                                                                                                                                                                                                                     227-7400
    9.5%;
29.3%;
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    Score 176; DB 5; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 209;
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                    Length 209;
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Matches

33

94

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US-08-920-440B-10
; Sequence 10, Application US/08920440B
; Patent No. 5919905
; GENERAL INFORMATION:
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US-09-609-324A-10
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SEQ ID NO 10
LENGTH: 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1995-10-03
PRIOR APPLICATION NUMBER: 08/318,393
PRIOR FILING DATE: 1994-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/920,440
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/538,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CERRETTI, Douglas P.
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/609,324A
CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: LERK-6
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                 APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
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                                                                                          STREET: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 VYWNSANKRFOA----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                    COUNTRY:
                                                                                                                                                    DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PNLVDRPCLR--LKVYVR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
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                                                                                                                                51 University Street
                                                                    USA
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                                                                                                                                                        Immunex Corporation
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36.8%; Pred. No. 2.3e
tive 14; Mismatches
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2.3e-07;
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US-09-173-492-10
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TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440B
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local
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                                                                                        NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826
TELECOMPUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                      TELEFAX: (206) 233-06 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION TATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
PILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                              SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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             amino acid
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51 University Street
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                                                                                                                                                                                                                                                              US/08/920,440
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Pred. No. 2.3e-07;
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; MOLECULE TYPE: US-09-173-492-10
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US-09-173-133-10
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Patent No. 6232447
GENERAL INFORMATION:
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                                                                                                                                                               Query Match
Best Local :
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: US/0:
PILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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tes 43; Conserv
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                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                            LENGTH:
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GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISAT 154
                                    QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                         VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
                                                                                                           VYWNSANKRFOA----EGGYVLYPOIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                              43;
                                                                                                                                          h 9.5%;
Similarity 36.8%;
43; Conservative 14
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51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/920,440
                                                                                                                                            14;
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                                                                                                                                            Score 175.5; DB 4;
Pred. No. 2.3e-07;
4; Mismatches 51;
                                                                                                                                                                               Length 213;
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RESULT 40

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GENERAL INFORMATION:

APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Hosmalu, Gezaldine
APPLICANT: Nosmalu, Gezaldine
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYROSINE KINASES
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.33USWO
CURRENT APPLICATION NUMBER: US/99/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08455001 Patent No. 5795734
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                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Flanagan, John G
APPLICANT: Cheng, Hwai-Jong
                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EPH Receptor TITLE OF INVENTION: Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 9.4%; Score 174.5; DB 4; Length 233;
Local Similarity 27.4%; Pred. No. 3.1e-07;
les 60; Conservative 24; Mismatches 74; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFHAGHEYYYISTPTHNLH------WKCLR--MKVFVCCASTSHSG---EKPVPTLPQF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVLYMVSRNGYRTCNASQGFKRWECNRPHAPH-----SPIKFSEKFORYSAFSLGY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEFYKLYLVG-----GAQGRR----CEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALG----NRHAVYWŃŚSNOHLRRE-GYTVOVNVNDYLDIYCPHYNSSGAGPGPGGGAE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP-- 185
                                                                                                                                                                                                                                                                                    Boston
                                                                                                                                                                                                                                                                 M
                                                                                                                                                                                                                                                                                                           E: LAHIVE & COCKFIELD
60 State Street
                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flanagan, John G.
INFORMATION:
                                                                 US/08/455,001
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PCT-US95-11869-4
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GENERAL INFORMATION:
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                                                                                                                                                     Matches
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELECHNEE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EPH Receptor Li
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: .
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 NLWGHEFRSHHDYYIIATS 141
                                                                                                                                                     Local Similarity 35.3 hes 49; Conservative
  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 ALLLIGVIGIVSGISIEP------VYWNSANKRFQAEGGYVLYPQIGDRIDLICPRA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 9.3%; Score 172; DB 1; Length 200; Local Similarity 35.3%; Pred. No. 4.1e-07; les 49; Conservative 16; Mismatches 58; Indels
                                                                                                              15 ALLILGVIGLVSGLSLEP------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
                                  66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE
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                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEPLP--AERMERYVLYMVNYEGHASCDHROKGFKRWECNRPDSPSGPLKFSEKFOLFTP 122
EEPLP--AERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLKFSEKFQLFTP 122
                                                                           AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVEVSINDYLDIYCPHY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application PC/TUS9511869
                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                 protein
                                                                                                                                                 9.3%; Score 172; DB 5; Length 200; 35.3%; Pred. No. 4.1e-07; ative 16; Mismatches 58; Indels
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08240124 Patent No. 5516658
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US 08/
FILING DATE: 03-DEC-1993
PRIOR APPLICATION UNWBER: US 08/
PILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
PILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SERSE XATHERYN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BECKMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CERRETTI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 NLWGHEFRSHHDYYIIATS 141
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                               142 DGTREGLESLQGGVCLTRGMXVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE 201
                                                                                                                                                     20
                                                                                                                                                                                      24 LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                             LVGGAQGRRCEAP-PAPNILLITCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                        MYDWPGYESCQAEGPRAYKRWYCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136
                                                                                                                                                   LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : SEATTLE
                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                       201 amino acids
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BECKMANN, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I, DOUGLAS P.
CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                                                                                                                                                                                                                9.2%; Score 169.5; DB 1;
29.9%; Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/161,132
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                                                                                                                                                                                                                               18; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2814-C
-RLQVSVCCKERKSESAHPV---- 164
                                                                                                                                                                                                                                                                   Length 201;
                                                                                                                                                                                                                                 Indels
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US-08-453-943-4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-193
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (200) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/161/132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION UNMBER: US 08/114,426
PILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202
137
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ITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
ITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 09-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/01
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                      83
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                                                                                                                                                                     24 LVSGLSL-EPYYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
                                                                                                                                                                                                                         Match 9.2%; Local Similarity 29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GSPGESGTSGWRGGDTPSP----
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 --TPE---
                                                                  MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136
                                                                                                  LVGGAQGRRCEAP-PAPNILITCDRPDIDIRFTIKFQEYSPNIWGHEFRSHHDYYIIATS 14:
                             DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE 201
                                                                                                                                       LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4, APP110
0. 5738844
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                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                   201 amino acids
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                                                                                                                                                                                                            Conservative
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 ---SSGQCL
                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                      4:
                                                                                                                                                                                                            18;
                                                                                                                                                                                                                            Score 169.5; DB 1
Pred. No. 6.7e-07;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LCLLLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version
 RLOVSVCCKERKSESAHPV---
                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                           Length 201;
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   164
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057.177
FILING DATE:
CLASCOTTON
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Patent No. 5969110
                                                                                                                                                                                Matches
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: US 08/161
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/114
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 2814
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: CERRETTI, DOUGI
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142 DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKÞVSEMÞMERDRGAAHSLEÞGKE 201
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                                                                                                                                            24 LVSGLSL-EPVYMNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
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                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136
                                                                               LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                             LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                                                                                                                                                66;
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                                                                                                                                                                                                                                                                                           amino acid
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CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
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                                                                                                                                                                              Score 169.5; I
Pred. No. 6.7e
18; Mismatches
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US-09-358-734-4
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Patent No. 6274117
GENERAL INFORMATION:
APPLICANT: BECKWANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: RECEPTOR HEK
TITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
PILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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 137
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                            142 DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMFMERDRGAAHSLEPGKE 201
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                                                                                                                                                                                               Local
                                                                                          83
                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                    24 LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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                                                                                          LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                        LRGGSSLRHVVYMNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                         MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136
                                                                                                                                                                                   ch 9.2%;
l Similarity 29.9%;
66; Conservative 1
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                                                                                                                                                                                  Score 169.5; DB 4;
Pred. No. 6.7e-07;
8; Mismatches 82;
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 -RLQVSVCCKERKSESAHPV---- 164
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US-09-214-631-8
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Best Local (
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APPLICANT: Holland, Sacha
APPLICANT: Hosmalu, Geraldine
APPLICANT: Mamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFF
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK
TITLE OF INVENTION: TROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
NUMBER: OF SEQ ID NOS: 13
NUMBER: OF SEQ ID NOS: 13
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; ORGANISM: Homo sapiens
US-09-214-631-8
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Patent No. 6413730
GENERAL INFORMATION:
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SEQ ID NO 8
LENGTH: 201
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Patent No. 6413730
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APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757,23USWO
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EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
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CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPPEGP--ETFALYMVDWPGYESCOAEGPRGYKRWVCSLPFGHVQFSEKIORFTPFSLGF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPHSSPNYEFYKLYLVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFLPGETYYYISVP--TPE----SSGQCL-----
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ilarity 29.8%;
Conservative 1
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Pred. No. 7.4e-07;
9; Mismatches 84; Indels
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RESULT 49
US-08-442-248-4
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Best Local S
Matches 65
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LENGTH: 209
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Patent No. 5759863
GENERAL INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOXChia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,2/
FILLING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
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                                                                                                                                                                                                                                                TYPE: ami: TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFPPGHEYYYISAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
    91
                                        86
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                                                                                                              33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG-----
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                          VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90
      DHTSKGFKRWECNRPHSPN---
                                    ----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94080
                                                                                                                                                   h 9.1%; Score 167.5; DB 1; Similarity 28.8%; Pred. No. 1.2e-06; 65; Conservative 29; Mismatches 81;
                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                    228 amino acids
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                                                                                                                                                                                                                                                linear
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  --GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS 141
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US-08-440-815-4
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Patent No. 5798448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION DATA:
APPLICATION UMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY, AGENT INFORMATION:
NAME: TOrchia, Timothy E.
REGISTRATION UMBER: 36,700
REGISTRATION UMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-8674
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187
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                                                                                                                                                                                                              34 VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90
                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C1
                                                                                                                                        91 DHTSKGFKRWECHRPHSPN------GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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                                  PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
                                                                                                      S---DGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                                                                                                                                                       ----GAQGRRCEAPPAPHLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIJAT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                                                   AIPDNGRRS-----CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE
PADDTV---HESAEPSRG-ENAAQTPRIPSRL--
                                                                                                                                                                                                                                                                                       65;
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T: 460 Point San Bruno
South San Francisco
California
                                                                                                                                                                                                                                                                                                      h 9.1%; Score 167.5; DB 1
Similarity 28.8%; Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                  228 amino acids
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 -LAILLFLLA 223
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Search completed: February 11, 2003, 12:06:26 Job time : 14.6918 secs

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Maximum Match 100%
Listing first 50 summaries
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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  Copyright
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  GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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LERK-7 precursor -
B61 protein precur
collagen alpha 1(X
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LERK-3 - human
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Stral/Eplg2 protei
LERK-2 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                      repulsive axon
LERK-4 - human
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143 7.7 1747 2 A54111 Collagen alpha-4 (V Collagen alpha 1 (V 142.5 7.7 1496 1 CGHUZV Collagen alpha 2 (V 142.5 7.7 1496 1 CGHUZV Collagen alpha 1 (V 142.5 7.7 1496 1 CGHUZV Collagen alpha 2 (V 142.5 7.7 142 2 S15435 Collagen alpha 2 (V 142.5 7.7 172.6 1466 1 CGHUZY Collagen alpha 2 (V 141.5 7.6 1466 1 CGHUZY Collagen alpha 2 (I 141.5 7.6 1466 1 CGHUZY Collagen alpha 1 (V 141.5 7.6 1466 1 CGHUZY Collagen alpha 1 (V 141.5 7.6 1466 1 CGHUZY Collagen alpha 1 (V 141.5 7.6 141.6 7.4 1 S23298 Collagen alpha 1 (V 141.5 7.6 141.6 2 T32482 Collagen alpha 1 (V 141.5 7.6 141.6 2 T32482 Collagen alpha 1 (V 141.5 7.6 141.6 2 T32482 Collagen alpha 1 (V 141.5 7.6 141.6 2 T32482 Collagen alpha 1 (V 141.5 7.6 141.6 2 T32482 Collagen alpha 1 (V 141.5 7.6 141.6 2 T32482 Collagen alpha 1 (V 141.5 7.6 141.6 2 T32482 Collagen alpha 1 (V 141.6 141.6 2 T32482 Coll	50	49	48	47	46	45	44	43	42	41	40	39	ա 8	37	36	ယ G	<u>ي</u>	LJ LJ	32	31	Ü
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2 A541182 2 A54125 1 CGHUZV 2 S15435 1 CGHUZV 2 S15436 2 S16366 1 CGHUZE 1 A24246 1 A23250 1 A34246 2 T722482 2 T72482 2 T72482 2 T72482 1 CGHULD 2 A44584 2 T72482 1 CGHULD 2 A44584 2 T72482 1 CGHULD 2 A44584 3 T80251 2 A1182 2 B41182 2 B41182	•				٠	٠		٠	٠	٠	•		•		•		•	•	•	•	•
A54121 A54121 A541779 CGHU2V S15435 S21369 S11366 CGHU7L T32250 A34246 A34246 A34246 S23298 T30165 T30165 T204182 CGHU1D B44984 J80291 S18251 A24450 A41182 B41182	1546	1487	1419	469	1024	940	210	680	304	305	744	744	319	1466	1763	1029	744	1496	743	1747	100
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collagen a	CGHU2E	B41182	A41182	A24450	\$18251	JE0291	B44984	CGHU1D	T22482	T30165	823298	A34246	T32250	CGHU7L	S16366	821369	815435	CGHU2V	S23779	A54121	
	collagen a			collagen a	lagen	FB19 prote		collagen a		hypothetic	collagen a	collagen a	hypothetic	collagen	collagen a	1					

ALIGNMENTS

RESULT

hepatoma transmembrane kinase ligand - mouse C;Species: Mus musculus (house mouse) C;Date: 02-U11-1996 #sequence_revision 02-Uu1-1996 #text_change 05-Nov-1999

C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 05-Nov-1999
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 05-Nov-1999
C;Accession: 149766
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthew Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the Eph-related receptor protein-tyrosine ki. A;Reference number: 149766; MUID:95199254; PMID:7534404
A;Reference number: 149766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecula type: mRNA
A;Residues: 1-336 <RESA;Residues: 1-340 <RESA;Residues Ś Ś 밁 Ś 밁 Ś 밁 A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678 C;Genetics: Ś よ 닭 გ C;Genetics: A;Gene: HTK Query Match 34.5%; Score 637.5; DB 2; Best Local Similarity 42.1%; Pred. No. 1.9e-37; Matches 139; Conservative 49; Mismatches 129; 311 194 134 191 134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190 17 74 74 GLLMVLCRTAISRSIVLEPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGGRGPREAEPGELGIALRGGGAADPPFCPH GRSSTTSPFVKFNPGSSTDGNSAGHSGNNLLGSEVALFÄGTÄSGCIIFIVIIITLVVLLL YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC Indels 13; Length 310 253 250 73 5

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hepatoma transmembrane kinase ligand - human C;Species: Homo sapiens (man) C;Species: 14-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999 C;Accession: 184743 C;Accession: 184743 R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995 A;Title: Molecular cloning of a ligand for the EpH-related receptor protein-tyrosine kin A;Reference number: 149766; MUID:95199254; PMID:7534404 A;Recession: 184743 A;Ccession: 184743 A;Reterin preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-333 cRES'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kin A;Reference number: S46993; MUID:94349923; PMID:8070404 A;Accession: S46993
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A; Residues: 1-346 <BEC>
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EMBO J. 13, 3757-3762, 1994
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C;Species: Homo sapiens (man)
C;Date: 15-Jul.1995 #sequence_revision
C;Accession: S46993
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Best Local S
Matches 145
                                                                                     :Gene: GDB:EPLG5; LERK5
:Cross-references: GDB:438338; OMIM:600527
Matches
               Query Match
Best Local Similarity
                                                                    position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD
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135;
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               34.0%;
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39.5%; Pred. No. 4.7e
tive 48; Mismatches
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 52
•
Score 629.5; DB 2;
Pred. No. 6.8e-37;
2; Mismatches 130;
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4.7e-37;
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                                                                                                                                          PID:g769676
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> SPNYEFYKLYLVGGAQGRRCBAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132 AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--

72

YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKY

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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 148780; ASS507; ASS062; S52670
R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, Dev. Biol. 170, 420-433, 1995
Bev. Biol. 170, 420-433, 1995
A;Reference number: 148780; MUID:95377533; PMID:7649373
                                                                                                                                       A;Status: preliminary; not compared with cor
A;Molecule type: mRNA
A;Residues: 1-89,'T',91-345 <SHA>
A;Crose-references: GB:U12983; NID:g575928;
C;Genetics:
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R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A;Title: cDNA cloning and characterization of a ligand for the A;Reference number: A55062; MUID:95014510; PMID:7929389
A;Accession: A55062
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859 R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, Genomics 24, 127-13, 1994 A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene A;Reference number: A55507; MUID:95203867; PMID:7896266
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A;Molecule type: DNA
A;Residues: 1-345 <FLE>
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A;Accession: A55507
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A; Residues: 1-345 < RES>
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Best Local
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ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS
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                                                             Similarity
                                            Conservative
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                                                             33.2%;
                                            51;
                                          Score 613.5; DB 2;
Pred. No. 9.3e-36;
1; Mismatches 107;
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                                              Indels
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                                              Gaps
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R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollin Oncogene 9, 3241-3248, 1994
A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conser A;Reference number: I58406; MUID:95022634; PMID:7936648
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
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RESULT 6
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Best Local Simi
Matches 137;
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Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999;
Accession: I58406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSLSTLASP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLLGVAGAGGA------MCWRRRRAKPSESRHPGPGSFGRGGSLGL----GG
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                                                                                                                                                                                                                                                 LLLIGVAGAGGA-----GG 279
                                                                                                                                                                                                                                                                                         VKT-----ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSK 236
                                                                                                                                                                                                                                                                                                                              AHSLEPGKENLPGDPTSNATSRGAEGP------LPPPSMPAVAGAAGG------LA 236
                                                                                                                                                                                                                                                                                                                                                                                          HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPNYMGLEFKKY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMVVITLCRLATPLAKNIEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK
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                                                                                             V 340
                                                                                                                                      KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK 344
                                                                                                                                                                         GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYK 339
                                                                                                                                                                                                                                                                                                                                                                     HDYYITSTSNGSLEGLENREGGYCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%;
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                                                                                                                                                                                                                RAAALSLSTLASP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g563119
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A;Molecule type: DNA
A;Residues: 1-237 <WIL>
A;Cross-references: EMBL:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8
A;Experimental source: clone C43F9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C43F9.8 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Accession: T19914
R.Mortimore, B.
                                                                                                                                                                                                                                                                                                                                                          A; Nolecule type: mRNA
A; Nolecule type: mRNA
A; Residues: 1-238 < RES>
A: Cross-references: EMBL: U14187; NID: g642832;
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A;Reference number: Z19195
A;Accession: T19914
A;Status: preliminary; translated
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A;Title: Ligands for the receptor tyrosine kinases hek and A;Title: Ligands for the receptor tyrosine kinases hek and A;Teference number: 138849; MUID:95140419; PMID:7838529
A;Accession: 138849
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C, Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                      A;Gene: GDB:EPLG3
A;Cross-references: GDB:438336; OMIM:601381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
C;Accession: 138849
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.;
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A; Introns: 32/2; 96/3; 214/1
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                                                                                                                            GPGGAKAGYTTTTGATGTRATTEBAKANKSVNKKŁOVEGCKATTTGTTTCE--K
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SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF
                                         ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                                                                                       h 9.7%; Score 179; DB 2; J
Similarity 28.4%; Pred. No. 1.4e-05;
65; Conservative 24; Mismatches 80;
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                                                                                     -GALG-----NRHAVYWNSSNOHLRRE-GYTVQVNVNDYLDIYCPHYN 67
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25.7%; Pred. No. 4.7e-08;
ative 41; Mismatches 83;
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                                                                                                                                                                                                                                                                                                                                                                        PIDN:AAC50078.1; PID:g642833
                                                                                                                                                                                                                   Length 238;
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                                                                                                                                                                            Gaps
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RESULT 8
A54984
A54984
ELF-1 protein precursor - mouse
N;Alternate names: Cek7 ligand
C;Species: Mus musculus (house mouse)
C;Date: 11:Nov-1994 #sequence_revision 11-Nov-1994 #text_change
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994
A;Title: Identification and cloning of ELF-1, a developmentally
A;Reference number: A54984; MUID:95007776; PMID:7522971
A;Reference number: A54984; MUID:95007776; PMID:7522971
                                                       R;Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T. Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, chromosal mapping, and tissue expression of A;Reference number: JE0322; MUID:99045414; PMID:9826538
A;Accession: JE0322
A;Status: preliminary
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C;Superfamily: axon guidance signal protein
C;Keywords: lipoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837 R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M. J. Biol. Chem. 270, 3467-3470, 1995
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A;Molecule type: mRNA
A;Residues: 1-209 <SHA>
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J.Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine A; Reference number: A55873; MUID:95181289; PMID:7876076
A; Accession: A55873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <CHE>
                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-213 <AAS>
                                                                                                                                                                                      C; Accession: JE0322
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                                                                                                                                                                                                                                                                          JE0322
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Best Local S
Matches 58
                                                                                                                                                                                                          ;Species: Homo sapiens (man)
;Date: 05-Feb-1999 #sequence
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                                                                                                                                                                                                                                                                                                                                                            EAPEPIFTSNSSCSGLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ----PNLVDRPCLR--LKVYVR
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58; Conservat
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  GB:AJ007292;
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NID: g3688367;
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Pred. No. 2e-05;
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  PIDN: CAA07435.1;
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  PID:g3688368
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repulsive axon guidance signal protein RAGS precursor - chicken C;Species: Gallus gallus (chicken) C;Cpate: 03-Nov-1995 #text_change 20-Jun-2000 C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000 C;Accession: A57084 R;Drescher, U; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonb Cell 82, 359-370, 1995
                                                     LERK-4 - human
(,Species: Homo sapiens (man)
(,Species: Homo sapiens (man)
(,Date: 29-May-1998 #sequence_revision 29-May-1998 #text_cha
(,Accession: I3885)
(,Accession: I3885)
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos,
Oncogene 10, 299-306, 1995
Oncogene 10, 299-306, 1995
A;Reference number: I38849; MUID:95140419; pMID:7838529
A;Reference number: I38850
A;Accession: I38850
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A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-201 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS
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                                                                                                                                                                                                                                                                                                                                       LATLLFLLAMLLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARPPGPHSSPNYEFYKLYLVG----
                                                                                                                                                                                                                                                                                                                                                                                                                          -PANSCMKTIGVHDRVFDVNDKVENSLEPADDTV---RESAEPSRG-ENAAQTPRIPIRL
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Pred. No. 2.2e-05;
4; Mismatches 51
                                            from GB/EMBL/DDBJ
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                                                                                                             isolation of cDNAs
                                                                                                                                                     Teepe, M.; Lyman,
                                                                                                                                                                                           29-Sep-1999
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A;Cross-references:
C;Genetics:
A;Gene: GDB:EPLG4
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A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein
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A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved A;Reference number: I58170; MUID:95267434, PMID:7748564
A;Accession: I58170
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A;Molecule type: mRNA
A;Residues: 1-228 <KOZ>
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R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, I
submitted to the EMBL Data Library, May 1995
A;Reference number: G08477
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A; Residues: 1-228 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: GDB:BPLG7; AF1; LERK7; ONIM:601535; Cross-references: GDB:568757; ONIM:601535; Map position: 13q33-13q33
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Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
Accession: I58170; G01812
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  142 AIPDNGRRS-
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                                                                                                        91
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                                                                                                                                                                                                                                                                    33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG------ 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
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                                                 S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                                                                                           DHTSKGFKRWECNRPHSPN
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                                                                                                                                                            ----GAQGRRCEAPPAPULLICORPOLDLRFTIKFQEYSPULWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                   VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
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                                                                                                                                                                                                                                                                                                                                                     9.1%;
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29.9%; Pred. No. 5.5e-05;
tive 18; Mismatches 82
  CLK--LKVFVR---
                                                                                                                                                                                                                                                                                                                        ; Score 167.5; DB 2; ; Pred. No. 8.7e-05; 29; Mismatches 81;
                                                                                                        -GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS 141
  - PTNSCMKTIGVHDRVFDVNDKVENSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLQVSVCCKERKSESAHPV-----
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                                                                                                                                                                                                                                                                                                                           51;
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                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-285; A',287-680 < ELI>
A; Residues: 1-285; A',287-680 < ELI>
A; Cross references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
A; Cross references: EMBL:X67348; NID:g50480; PiDN:CAA47763.1; PID:g50481
A; Elima, K.; Metsaerants, M.; Kallio, J.; Peraelae, M.; Berola, I.; Garofalo, S.; de
Blochim. Biophys. Acta 1130, 78-80, 1992
A; Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen
A; Reference number: S22215; MUID:92182017; PMID:1543751
A; Accession: S22215
                 A;Status: preliminary
A;Molecule type: mxNA
A;Residuse: 385-450, 'K', 452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:SA;Apple, S.S.; Olsen, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.
MOI. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium A;Reference number: A36377; MUID:91042512; PMID:2233719
A;Accession: A36377
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; PID:g49794
R;Elima, K.; Berola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and A;Reference number: S28807; MUID:93143676; PMID:8424763
A;Accession: S28807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text change 13-Aug-1999 C;Accession: S31216; S28071; S32215; S30127; I48299; S26397; S31830 R;Kong, R,Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; (Eur. J. Blochem. 213, 99-111, 1993 Brantive use of promoter and expression of the mouse A;Reference number: S31216; MUID:93238750; PMID:8477738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Accession: A36377
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A36377
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A;Residues: 1-205 <HOL>
A;Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321
C;Superfamily: axon guidance signal protein
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A; Residues: 1-680 < KON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76
S.S.; Olsen, B.R
13, 165-179, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
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                                                    NID: g49795;
                                                      PIDN: CAA44741.1;
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                                                         PID: 949796
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A; Rolecule Cype: LWA
A; Residues: S2-247; L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'A; Cross-references: RMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
R; Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
J. Biol. Chem. 263, 581-587, 1988
A; Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibod A; Reference number: $26397; MUID:88087150; PMID:2826450
A; Accession: $26397; MUID:88087150; PMID:2826450
A; Ancession: $26397; MUID:880
collagen alpha 1(III) chain - bovine (Species: Bos primigenius taurus (cattle) (?Species: Bos primigenius taurus (cattle) (c;pate: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 07-May-1999 (c;pate: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 07-May-1999 (c;pate: 04-Dec-1986 #sequence revision; A38003; A38004; A38005; S71946 (c;pate: 04-Dec-1986) A38004; A38004
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A;Residues: 1-12, F',14-26, S',28-247,'I',249-285,'A',287-305,'F',307-416,'S',418-499,'I
A;Residues: S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
Eyr. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse the A;Reference number: 148299; MUID:92267014; PMID:1587271
A;Accession: 148299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSPNLWGHEFRSHHDYYIIATSDGT----REGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GAPGPAGIATKGLNGPTGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRGPVGPVGAKGVPGHNGEAGPR-GEPGIPGTR---
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25.5%;
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Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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F;15-1040/Region: helical
F;507-589/Region: cell attachment (R-G-D) motif
F;527-549/Region: cell attachment (R-G-D) motif
F;875-877/Region: cell attachment (R-G-D) motif
F;875-877/Region: cell attachment (R-G-D) motif
F;879-880/Region: cell attachment (R-G-D) motif
F;935-937/Region: cell attachment (R-G-D) motif
F;107,119,938,950/Modified site: 5-hydroxylypine (Lys) #sterminal monhelical telopeptide
F;107,119,938,950/Modified site: 5-hydroxylypine (Lys) #sterminal monhelical telopeptide
F;107,950/Modified site: allysine (Lys) #sterminal meredicted
F;107/Binding site: carbohydrate (Lys) (covalent) #status predicted
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A;Molecule type: protein
A;Residues: 243-422 <DEW1>
R;Bentz, H.; Fietzek, P.P.; Kuehn, K.
R;Bentz, H.; Fietzek, Fietzek, P.P.; Kuehn, K.
R;Bentz, H.; Fietzek, Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are C;Comment: The type III collagen molecule is a trimer of identical chains, linked to ea C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology C;Keywords: colled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol F;1-1049/Product: collagen alpha 1(III) chain #status experimental <CABs F;15-104/Region: mmino-terminal nonhelical telopeptide F;15-104/Region: cell attachment (R-G-D) motif F;857-889/Region: cell attachment (R-G-D) motif F;875-877/Region: cell attachment (R-G-D) motif F;875-877/Region: cell attachment (R-G-D) motif F;875-877/Region: cell attachment (R-G-D) motif
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A;Accession: A38002
A;Molecule type: protein
A;Residues: 423-571 <BEN>
R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A;Title: The covalent structure of calf skin type III of A;Reference number: A38003; MUID:80026029; PMID:488909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S71946
A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
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A;Title: Cross-link analysis of the C-telopeptide domain A;Reference number: S71946; MUID:96404897; PMID:8809038
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A; Accession: A38005
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Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868,
A;Title: The covalent structure of calf skin ty
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Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A;Tille: The covalent structure of calf skin type III of A;Reference number: A38004; MUID:80026030; PMID:488910
A;Accession: A38004
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Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A;Title: The covalent structure of calf skin type III.
A;Reference number: A38001; MUID:80026027; PMID:488907
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A; Residues: 572-808 <LAN>
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A; Residues: 809-947 < DEW2 >
                                                                                                                                                          Query Match
Best Local S
Matches 60
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PAGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGGRGPPGFPGSNGNPGPPGSSGAPGKDG
                                                                                 PRGGAVPRKPVSEMPMERDRGA----
                                                                                                                                                                                                      Similarity
                                                                                                                                                      8.4%;
nilarity 26.5%;
Conservative
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                                                                                                                                                          Score 154.5; DB 1;
Pred. No. 0.0036;
Pred. No. 74;
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A;Residues: 1-1670 <MAR>
A;Cross-references: GB:X80031; NID:g577563; PID:g577564
A;Experimental source: kidney
A;Experimental source: kidney
A;Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey,
J. Clin. Invest. 89, 592-601, 1992
A;Title: Molecular cloning of the human Goodpasture antigen demonstrates it
A;Reference number: A43928; MUID:92147878; PMID:1737849
A;Accession: A43928
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:g177896
A;Note: sequence extracted from NCBI backbone (NCBIP:115597)
R;Quinones; S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358, 1994
A;Reference number: A44738; NUID:94274734; PMID:8006044
A;Contents: annotation; erratum; correction to intronic sequence in A4404
R;Bernal, D.; Quinones, S.; Saus, J.
J. Biol. Chem. 268, 12090-12094, 1993
A;Title: The human mRNA encoding the Goodpasture antigen is alternatively
A;Reference number: A45971; MUID:93280184; PMID:8505332
A;Accession: A45971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence revision 03-Oct-1995 #text change 22-Jun-1999
C;Accession: A54763; A43928; Ā44043; A45971; A39786
R;Mariyama, M.; Leimonen, A.; Mochizuki, T.; Tryggvason, K.; Reeders, S.T.
J Biol. Chem. 269, 23013-23017, 1994
A;Title: Complete primary structure of the human alpha3(IV) collagen chain.
A;Reference number: A54763; MUID:94364994; PMID:8083201
A;Accession: A54763
                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIP:133363); R;Morrison, K.E.; Mariyama, M.; Yang-Feng, T.L.; Reeders, S.T. Am. J. Hum. Genet. 49, 545-554, 1971. Hum. Genet. 49, 545-554, 1971. Partial cDNA encoding A;Title: Sequence and localization of a partial cDNA encoding A;Reference number: A39786; MUID:91353570; PMID:1882840 A;Accession: A39786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: kidney
R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.;
J. Biol. Chem. 267, 19780-19784, 1992
A;Title: Exon/intron structure of the human alpha 3(IV) ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1331-1524,'I',1526-1670
A;Cross-references: GB:M81379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen alpha 3(IV) chain precursor, long splice form N;Alternate names: Goodpasture antigen; procollagen alp
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A;Molecule type: mRNA
A;Residues: 1453-1593, A',1595-1670 <MOR>
A;Residues: 1453-1593, NID:g234418; PIDN:AAB19637.1;
A;Cross-references: GB:S55790; NID:g234418; PIDN:AAB19637.1;
C;Comment: Prolines and lysines at the third position of the ed and subsequently O-glycosylated.
C;Comment: In Goodpasture's syndrome, an autoimmune response
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A; Residues: 1386-1670 <QUI>
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A; Residues: 1427-1444 <BER>
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alpha 3(IV)
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F;1154-1156/Region: cell attachment (R-G-D) motif
F;1306-1308/Region: cell attachment (R-G-D) motif
F;1306-1308/Region: cell attachment (R-G-D) motif
F;1345-1347/Region: cell attachment (R-G-D) motif
F;1432-1434/Region: cell attachment (R-G-D) motif
F;1439-1670/Domain: carboxyl-terminal nonhelical, NC1 <NC1>
F;1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>
F;1451-1651/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;31,33,39,41,125,422,476,479,682,722,809,1387/Disulfide bonds: interchain #status
F;253/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1505-1511,1616-1622/Disulfide bonds: (or 1460-155, 1493-1548) #status predicted
F;1570-1662,1604-1665/Disulfide bonds: #status predicted
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C;Keywords: alternative splicing; basement membrane; cell binding; coiled coil; extrace
E;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1670/product: collagen alpha 3(IV) chain, long splice form #status predicted <MAT>
F;29-42/Domain: amino-terminal nonhelical, NH1 <NH1>
F;43-1438/Region: interrupted helical
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A;Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete
A;Introns: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strands wit
A;Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 3
mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric
er associations in the interrupted helical domain (with disulfide and desmosine cross-l
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Best Local
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1306 RGDPGF-QGFPGVKGEKGNPGFLGSIGPPGPIGPKGPPGV 1344
                                                                                                                                                                                                                                                                                                                                                                       1154 RGDQG-RDGIPGPAG----EKGETGLLRAPPGPRGNPGAQGAK-----GDRGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GPPHSGPGG-----VRVGALLLLGVLGLVSGLSLEPVYWNSANKR----FQAEGGYVLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIHGLQGDKGE---PGYSEGTRPGPPGPTGDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGPAGPEGAPGSPGSPGLPGKPGPHGDLGFKGIKGLLGPPGIRGPPGLPGFPGSPGPMGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPP--GPRGDLGSTGNPGEPGLLGIPGSMGNMGMP----GSKGKRGTLGFPGRAGRPGLP
                                                          AADPPFCPHYEKVSGDYGHPVYIVQDGP-----PQSPPNI
                                                                                                                         SPGAPGPPGPPGSHVIGIKGDKGSMGHPGPKGPPGTAGDMGPPGRLGAPGTPGLP--
                                                                                                                                                                                                                                                                                                         EPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRG--GAVPRKPVSEMPMERDRGAAHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----APPAPNL--LITCORPOLDLRFT-IKFQEYSPNLWGHE----FRSHHDYYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QI---
                                                                                                                                                                                       KPSESRHPGP---
                                                                                                                                                                                                                                                     - PGFPGLPG----RKGAMGDAGPRGPTGIEGFPGPPGLPGAIIPGQTGNRGP---PGSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GDRLDLLCP----RARPPGPHSSPNYEFYKLYLVGGAQGRRCE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%;
27.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Mismatches
                                                                                                                                                                                   GSFGRGGSLG-LGGGGGMGP--REAEPGELGIALRGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 153.5; DE Pred. No. 0.007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LPGDMGKKGEMGQPGPPGH 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1670;
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two alpha 3
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collagen 2 - Caenorhabditis elegans () Species: Caenorhabditts elegans () Species: Caenorhabditts elegans () Joun-1989 #Bequence revision 30-Jun-1989 () Accession: B31219; T37289; T26033; T37288 R;Kramer, J.M.; Cox, G.N.; Hirsh, D.

#text_change

R;Kramer, Cell 30,

599-606,

```
A;Cross-references: EMBL:AF022985; PIDN:AAB69961.1; GSPDB:GN00023; CESP:T15B7.4
A;Experimental source: strain Bristol N2; clone T15B7
C;Genetics:
                                                                                                                                                                                                                                                    R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, September 1997
submitted to the sequence of C. elegans cosmid T15B7
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
T32248
                                                                                                                                                                                                                     A;Description: The sequence of A;Reference number: Z21139 A;Accession: T32248
                                                                                                                                                                                                                                                                                                                         C; Date: 29-Oct-1995
C; Accession: T32248
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R;Kramer, J.M.; Cox, G.N., Hirsh, D.
J. Biol. Chem. 260, 1945-1951, 1985
J. Title: Expression of the Caenorhabditis elegans collagen genes
A;Reference number: Z21668; MUID:85105075; PMID:2578467
A;Recession: T37288
A; Introns: 266, C; Superfamily:
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-325 < PAU>
                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T15B7.4 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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A; Introns: 94/1
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A; Residues: 1-301 <K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-301 < KRA>
                                        A; Map position:
                                                                   A; Gene: CESP:T15B7.4
                                                                                                                                                                                               A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:J01048; NID:g156261; PIDN:AAA27990.1; PID:g156262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-301 <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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A;Accession: T26033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-301 <KR3>
A;Cross-references: EMBL:V00148; NID:g6683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tille: Comparisons of the complete sequences of two collagen genes from Caenorhabditis
;Reference number: A90826; MUID:83050944; PMID:7139711
;Accession: B31219
                                                                                                                                                                                                                                                                                                                                                      ;Date: 29-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 GQSPRGGAVPRKFVSEMPMERDRG------AAHSLEPGKENLPGDPT--SNATSRGAE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGTGGPGPAGPKGPPGAAGAPGADGNPGGPGTAGKPGGEGEKGICPKYCAIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLGLGGGGGMGPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPAGPAGNDGAPGAPGG-----PGEPGASEQGGP-----GEPGPAGPPGPAGPAGNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPLPPPSMPAVAGAAGGLALLLLGVAGA----GGAMCWRRRRAKPSESRHPGP-GSFGRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNPGKGASAPCEPVTQPPCQPCPGGPPGPAGPAGPPGPPGPDGNPGSPAGPSGPGPAGPP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; translated
                     266/1
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  unassigned
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28.7%; Pred. No. 0.0015;
"F. Mismatches 72;
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  collagens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA23464.1;
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C;Species: Bombyx mor
C;Date: 06-Jan-1995 #
C;Accession: S42886
R;Chareyre, P.P.; Bes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, March 1994
A;Description: A novel collagen encoding mRNA is transiently accumulated A;Reference number: $42886
A;Status. Transient S42886
A;Status. Transient S42886
                            hypothetical protein F02D10.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex C;Accession: T20497 R;Swinburne, J.
                                                                                                                      RESULT
T20497
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-reterence unassigned C;Superfamily: unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-569 <CHA>
A;Cross-references: EMBL:Z30348; NID:g457768; PIDN:CAA83002.1; PID:g457769
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submitted to the EMBL Data A; Reference number: Z19283
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Best Local Similarity 26.0
Matches 92; Conservative
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                                                                                                                                                                                                                              GPREAEPGELGIALRG----GGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPAGAPGPAGP-----PGA----PGPKGNNGQPGAPAQS-GGRGP-PGPRGP--A
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                                                                                                                                                                                            PGQPGQPGQQGYPGQGGPQQGGQPINPSQPGYPGQSGQPGYPGQPVQPGQPGQP
                                                                                                                                                                                                                                                                  QÁG-----QPGYPGQGG-----QPIKPAQPGHPGQPGQPGQPGTPGQPGQPGYPGQPGQ
                                                                                                                                                                                                                                                                                                   AAGGLALLLIGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLGLGGGGGGM 283
                                                                                                                                                                                                                                                                                                                                       PGQGGQPIKPGQ------PGYPGQPGQPGQPGYPGQP-GQPGAPGQPGQPGQPGQPGTPG 50
                                                                                                                                                                                                                                                                                                                                                                       PRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGP-AGGPGQPG---HSGGAGSPGPQGP----PGPSGQPGHSGNDGVPGAPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GPREASPGELGIALRGGGAADP-PFCPHYEKVSGDYGHPVYIVQDGPPQSPPN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGG--SLGLGGGGGM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLLRVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRARPPGPHSSPNYEFYKLYLVG------GAQGRRCEA-PPAPNLLLTCDRPDLDL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSASTLVTVASAASGIAIVVCVFTVGMIFNDINSFYDEKIGELKEFKGYEQIA--WQAMI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PGQPGAPGEQGHPG-----LAGQPGSGARINPATGRPGFCIT------
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                Library,
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Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 149; DB 2;
Pred. No. 0.0045;
4; Mismatches 7'
                  November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPGQPGHPGSPGNPGRGGQRSRGLPGPSGRPGP
                                                                   #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 569
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R;Rokos, I.; Muragaki, Y.; Warman, M.; Olsen, B.R. Matrix Biol. 14, 1-8, 1994
A;Title: Assembly and sequencing of a cDNA coverin A;Reference number: $42617; MUID:94340199; PMID:80 A;Accession: $42617
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C;Species: Musculus (house mouse)
C;Date: 25-Dec.394 #sequence_revision 19-Apr-1996 #text_change 20-Sep-1999
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A;Molecule type: DNA
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Best Local S
Matches 87
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                    MPGTKGEAGKPGPPGDVGIAGLPGVPGIPGAKGVAGEKGNTGAPGKPGQLGSSGKPGQQG
                                                                                                                                                                                                                                                                                                                                         GIPGAAGDQGQRGPPGETGPEGDRGI-----QGSRGIPGSPGPKGDTGLPGVDGRDGIPG
                                                                                                                                                                                                                                                                                                                                                                                                                           AVP-----RKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATS--RGAEGPLPPPS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PGRQGHKGEEGDQGELGEVGDQGPPGPQGLRGITGIVGDKGEKGARGFDGEPGPQ 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPNSCPPGRSGYPG-----LPGMRGHKGAKGEIGE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGSAGGPGPKGPPGPAGQPGSDGNPGTAGPPGNPGGEGEKGICPKYCAIDG 305
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    PPGEVGPRGPRGLPGSRGPVGPEGSPGIPGKLGSVGSPGLPGLPGPPGLPGMKGDRGVFG
                                                                                  -PGSFGRGGSLGL-GGGGGMGPREAE--PGELGIALRGG--GAADPPFCPHYEKVSGDYG 319
                                                                                                                                                                                                                                                       MPAVAGAAG-----GLALL--LLGVAGAGGAMCWRRRRAKPSE-----SRHPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLLRVGQSPRGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPRARPPGPHSSPNYEFYKLYLVG-----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIK 116
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24.0%; Pred. No. 0.009;
ive 23; Mismatches 130; Indels 1
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Pred. No. 0.00:
12; Mismatches
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A; Molecule type: mRNA
A; Residues: 28-687, 'L', 689-734,'F', 736-751,'R',753-1315 <OHW>
A; Cross-references: EMBL:L22545; NID:g348968; PIDN:AAA19787.1; PID:g511298
A; Ch. S.-F.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994
A; Title: Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xa.
A; Reference number: A58370; MUID:94240111; PMID:8183893
A; Accession: S65595
                                                                                                                                                      r;364-437/Domain: collagenous #status predicted F;462-583/Domain: collagenous #status predicted F;607-689/Domain: collagenous #status predicted F;704-745/Domain: collagenous #status predicted F;759-831/Domain: collagenous #status predicted F;759-831/Domain: collagenous #status predicted F;842-874/Domain: collagenous #status predicted F;842-874/Domain: collagenous #status predicted F;848-910/Domain: collagenous #status predicted F;892-894/Region: cell attachment (R-G-D) motif F;918-969/Domain: collagenous #status predicted F;918-969/Domain: collagenous #status P;918-969/Domain: collagenous #s
                                                                                                                                                                                                                                                  F;26-1315/Product: collagen alpha 1(XVIII) chain, show F;327-353/Domain: collagenous #status predicted <CO2>F;327-353/Domain: collagenous #status predicted <CO2>F;462-583/Domain: collagenous #status predicted <CO3>F;607-689/Domain: collagenous #status predicted <CO4>F;704-745/Domain: collagenous #status predicted <CO5>F;709-817/Domain: collagenous #status predicted <CO6>F;759-831/Domain: collagenous #status predicted <CO6>F;842-874/Domain: collagenous #status predicted <CO7>F;887-910/Domain: collagenous #status predicted <CO8>F;887-910/Domain: collagenous #status predicted <CO8-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixer-Pixe
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C;Comment: Prolines and lysines at the third position of the tripeptide repeating C;Comment: Brown the different splice forms of collagen alpha 1(XVIII) may be involved C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the actic applies the setul in treating solid tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U11636; NID:g618427; PIDN:AAC52178.1; PID:g618428 R;Rehn, M.; Pihlajaniemi, T. Proc. Natl. Acad. Sci. U.S.A. 91, 4234-4238, 1994 A;Title: Alpha1(XVIII), a collagen chain with frequent interruptions in the collagenous A;Reference number: A58371; MUID:94240112; PMID:8183894 A;Accession: A58371
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J. Biol. Chem. 270, 4705-4711, 1995
A;Title: Identification of three N-terminal ends of type
tif homologous to rat and Drosophila frizzled proteins.
A;Reference number: A56101; MUID:95181468; PMID:7876242
A;Accession: A56101
                                             F;1132-1315/Product: endostatin #status pr;1139-1315/Region: multiplexin collagen
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A; Residues: 28-1315 < OHS >
                                                                                                                           F;983-1000/Domain: collagenous #status predicted
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C; Superfamily: unassigned collagens
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A; Residues: 1-928 < REH2>
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A; Residues: 1-103 < REH1>
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F;126,488/Binding site: carbohydrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly, 1-25/Domain: signal sequence #status predicted <SIG>;24-235/Region: thrombospondin amino-terminal similarity;26-1315/Product: collagen alpha 1(XVIII) chain, short splice form #status predicted 
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A;Note: this sequence is presented as substitutions relative to another sequence in a file strong the sequence is presented as substitution of the sequence figure was reconstructed cysuperfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Keywords: colled coil; extracellular matrix; glycoprotein; trimer; triple helix F;37-96/Domain: von Willebrand factor type C repeat homology <VWC>F;1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1'(II) chain precursor - African clawed frog C;Species: Kenopus laevis (African clawed frog) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change C;Accession: A40333 # R;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
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A,TITLe: Expression of two nonallelic type
A,Reference number: A40333, MUID:92011898,
A,Recession: A40333
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A;Molecule type: mRNA
A;Residus; 1-1492 <SUA>
A;Cross-references: GB;M63596
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ell 88, 277-285, 1997
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239 GAGGPMGPRGPPGPSGKPGDDGEAGKPGKSGERGPPGPQGARGFPGTPGLPGVKGHRGYP
298
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R;Rehn, M.; Pihlajaniemi, T. 1995

J. Biol. Chem. 270, 4705-4711, 1995

A;Title: Identification of three N-terminal ends of type XVIII collagen chains tif homologous to rat and Drosophila frizzled proteins.

A;Reference number: A56101; MUID:95181468; PMID:7876242

A;Accession: B56101 C;Species: Mus musculus (house mouse)
C;Date: 03-Oct-1995 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
C;Accession: B56101; C56101; S72450; S65595; PN0675; A54072; A58816 A; Molecule type: mRNA collagen alpha 1(XVIII) oha 1(XVIII) chain precursor, l collagen alpha 1(XVIII) chain long long splice precursor, form medium splice PID:g618430 form; endostatin and tis

A;Accession: C56101

A;Residues: 1-562 <REH1>
A;Residues: 1-562 <REH1>
A;Cross-references: GB:Ul1637; NID:g618429; PIDN:AAC52179.1;
A;Experimental source: splice form clone PE17.24

A; Molecule type: mRNA
A; Residues: 1-239,487-562 < REH2>
A; Crose-references: GB:Ul1637; NID:g618429
A; Experimental source: splice form clones PE8.1,
R; Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons,
submitted to the EMBL Data Library, August 1993
A; Reference number: S72450
A; Accession: S72450

PE19, r.. s.; Ooshima, A.; Olsen, œ , 1524-1

A;Molecule type: mRNA
A;Residues: 487-1146,'L',1148-1193,'F',1195-1210,'R',1212-1512,'L',1514-1522,'F',
A;Residues: 487-1146,'L',1148-1193,'F',1195-1210,'R',1212-1512,'L',1514-1522,'F',
A;Cross-references: EMBL:L22545, NID:g348968; PIDN:AAA19787.1; PID:g511298
R;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994
A;Title: Isolation and sequencing of cDNAs for proteins with multiple domains of A;Reference number: A58370; MUID:94240111; PMID:8183893 A; Molecule type: mRNA A; Residues: 487-1512, 'L',1514-1522, 'F',1524-1683, 'V',1685-1774 A;Accession: S65595 Gly-Xa

A,Cross references: EMBL:122545

R;Abe, N.; Muragaki, Y.; Yoshioka, H.; Inoue, H.; Ninomiya, Y.
Blochem. Biophys. Res. Commun. 196, 576-582, 1993

A;Title: Identification of a novel collagen chain represented A;Reference number: PN0675; MUID:94059075; PMID:8240330

A;Accession: PN0675

A;Accession: PN0675

A;Molecule type: mRNA

A;Residues: 635-1774 <ABE>
R;Rehn, M.; Hintikka, E.; Pihlajaniemi, T.

U. Biol. Chem. 269, 13929-13935, 1994 γģ extensive interruption

of the alphai chain of mouse

A;Releterer TASA072
A;Accession: A54072
A;Molecule type: DNA; mRNA
A;Residues: 1293-1403,'R',1405-1774 <REH3>
A;Cross-references: GB:U03714; NID:g487733; PII
A;Cross-references: GB:U03714; NID:g487733; PII A; Title: Primary structure collagen chain. A; Reference number: A54072; MUID: 94245707; PMID:8188673 PIDN:AAA20657.1; ai, N.; Vasios, G. type PID: 9487734 XVIII collagen, partial

G.;

Lane, tumor

W.S.;

Flynn,

Η .

S

A; Reference number: A58816; A; Title: Endostatin: endogenous inhibitor of angiogenesis 816; MUID:97160848; PMID:9008168

A; Accession: A58816

position of the tripeptide repeating unit

A; Molecule type: protein
A; Residues: 1591-1610 <ORE>
A; Resperimental source: hemangioendothelium cells
A; Note: inhibits endothelial cell proliferation
C; Comment: Prolines and lysines at the third position of
lated and subsequently O-glycosylated.
C; Comment: The different splice forms of collagen alpha
C; Comment: Endostatin is released from collagen alpha
C; De useful in treating solid tumors. C;Genetics: A;Gene: MGI:Coll8a1 ha 1(XVIII) 1(XVIII) c may chain bg be the actio n per of t

MGI:71175

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C.Superfamily: unassigned collagens
C.Superfamily: unassigned collagens
C.Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteoglyd
F;1-1774/Product: collagen alpha 1(XVIII) chain precursor, long splice form #status pred
F;1-239,487-1774/Product: collagen alpha 1(XVIII) chain precursor, medium splice form #s
F;1-24/Domain: signal sequence #status predicted <C001>
F;361-486/Region: frizzled similarity
F;786-812/Domain: collagenous #status predicted <C002>
F;231-104/Domain: collagenous #status predicted <C003>
F;106-812/Domain: collagenous #status predicted <C004>
F;101-129/Domain: collagenous #status predicted <C006>
F;1218-1290/Domain: collagenous #status predicted <C006>
F;1311-133/Domain: collagenous #status predicted <C008>
F;136-1369/Domain: collagenous #status predicted <C008>
F;137-1429/Domain: collagenous #status predicted <C009>
F;1346-1369/Domain: collagenous #status predicted <C009>
F;1442-1459/Domain: collagenous #status predicted <C009>
F;1591-1774/Product: endostatin #status predicted <C009>
F;1591-1774/Product: endostatin #status predicted <C009>
F;1598-1774/Product: endosta
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A; Introns: 1;
A; Note: the ]
C; Superfamily
C; Keywords: 5
F; 1-1774/Proc
Collagen alpha 3(IX) chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change :
C;Accession: S20819; S22429; S22918; S22238; C18856; S22241
R;Brewton, R.G.; Ouspenskaia, M.V.; van der Rest, M.; Mayne, R.
Eur. J. Biochem. 205, 443-449; 1992
A;Title: Cloning of the chicken alpha-3(IX) collagen chain compl.
A;Reference number: S20819; MUID:92241276; PMID:1572350
A;Accession: S20819
A;Molecule type: mRNA
A;Residues: 1-675 <BRE>
A;Cross-references: EMBL:X64712; NID:g63316; PIDN:CAA45967.1; PII
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           Cross-references: EMBL:X64712; NID:g63316; PIDN:CAA45967.1; PID:g63317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDMEGS-GIPLWTTARSSDGLQGPPGSP 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVSGDYGHPVYIVQ-----DGPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GDVGIPGPKGSKGDLGPIGMPGKSGLA---GSPGPVGPPGPPGPPGPPGPPGFAAGF 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAKPSESRHPGP-GSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG--GAADPPFCPHY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGPAGLPGVP-----GKEGPPGFPGPPGPPGKEGP----PGVAGQKGSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGKENLPGDPTSNATSRGAEGP--LP-PPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP--VSEMPMERDR-GAAHSLE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----APPAPNLLICDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCPRAR-PPGPHSSPNYEFYKLYLVGGAQGRRCE------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPP--GPAGPQ------GPAGPVVQSPNSQPV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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23.7%;
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A;Molecule type: protein
A;Residues: 540-548 <MAY>
R;Ninomiya, Y.; van der Rest, M.;
A;Ninomiya, Y.; van der Rest, M.;
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F;22-675/Product: collagen alpha 3(IX) chain #status predicted <MAT>
F;22-24/Domain: non-collagenous NC4 #status predicted <CC4>
F;25-161/Domain: collagenous CC13 #status predicted <CC13>
F;162-176/Domain: non-collagenous NC3 #status predicted <CC13>
F;177-515/Domain: collagenous NC12 #status predicted <CC12>
F;516-546/Domain: non-collagenous NC2 #status predicted <CC12>
F;547-657/Domain: collagenous NC2 #status predicted <CC11>
F;548-675/Domain: non-collagenous NC2 #status predicted <CC11>
F;658-675/Domain: non-collagenous NC1 #status predicted <CC11>
F;658-675/Domain: non-collagenous NC1 #status predicted <NC1>
F;137,143,146,149,153,155,179,182,185,552,558/Modified site: hydroxyproline
F;170,174,525,658,663/Disulfide bonds: interchain #status predicted
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A;Residues: 1-195,'G','197-405,'S',407-675 <HA2>
A;Residues: 1-195,'G','197-405,'S',407-675 <HA2>
A;Cross-references: BMBL:M83179; NID:g211040; PIDN:AAB59960.1;
R;Mayne, R.; van der Rest, M.; Ninomiya, Y.; Olsen, B.R.
Ann. N. Y. Acad. Sci. 460, 38-46, 1985
A;Title: The structure of type IX collagen.
A;Reference number: S22238; MUID:86185164; PMID:3868958
A;Accession: S22238
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A;Note: 353-Arg, 386-Leu and 548-Arg were also found
R;Har-El, R.; Sharma, Y.D.; Agullera, A.; Ueyama, N.; Wu, J.J.; Eyre, D.R.;
submitted to the EMBL Data Library, February 1992
A;Description: Cloning and developmental expression of the alpha 3 chain of
A;Reference number: S22918
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A;Title: The structure and macromolecular organization of type IX coll. A;Reference number: $22241; MUID:90247791; PMID:2186687
A;Accession: $22241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 24, 4223-4229, 1985
A;Title: Construction and characterization of cDNA encoding the alpha2 chain A;Reference number: A18856; MUID:86026268; PMID:2996593
A;Accession: C18856
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A;Title: Cloning and developmental expression of the alpha3 chain of chicken type A;Reference number: S22429; MUID:92250566; PMID:1577778
A;Accession: S22429
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A; Residues: 1-195, 'G', 197-675 <HAl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 135, 'E', 137-187, 'X', 189-191 <SHI>
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A; Residues: 540-558 <NIN>
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   PGPPGPPGMPGFKGHTGHKGEPGEIGKEGEKGSPGPPGPPGI
                                                                                                                                                                                                                                                                                                      PAVAGAAG---GLALLLLGVAGAGGAMCWRRRRAKPSESRHPG------PGSFGRG-
                                                          -GAADPPFCPHYEKVSGDYGHPVYIVQDGP-----PQSPPNI 336
                                                                                                                         PGPPGPPGPSGLPGGNGFRGPPGPSGLPGFPGPPGPPGLAGIIPEGGGDLQCPALCP 175
                                                                                                                                                                                                                                              PGAAGEAGLPGLP----GVDGLTGT-----DGPPGPNGPPGDRGALGPAGPPGPAGKGL
                                                                                                                                                                                                                                                                                                                                                                       RVG--PQGPPGPRGPPGPSGKDGIDG----
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Pred. No. 0.0089;
9; Mismatches 71
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RyKoMurray, A.
RyKoMurray, A.
submitted to the EMBL Data Library,
perference number: Z19345
                                                                                                                       R;Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P. Blochem. J. 273, 141-148, 1991
A;Title: Isolation of cDNAs encoding the complete sequence of A;Reference number: S13301; MUID:91113131; PMID:1703407
A;Accession: S13301
                                                                                                                                                                                                             collagen alpha 1(X) chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
C;Accession: S13301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3
A;Introns: 27/3; 49/3
C;Superfamily: unassigned
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A;Gene: COL10A1
C;Superfamily: col:
C;Keywords: coiled
                                                                     A;Molecule type: mRNA
A;Residues: 1-674 <THO>
A;Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
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A;Residues: 1-305 <WIL>
A;Cross-references: EMBL:Z81503; PIDN:CAB04111.1; GSPDB:GN00021; CESP:F14F7.1
A;Experimental source: clone F14F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z19345
A;Accession: T20906
A;Status: preliminary; translated
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Best Local S
Matches 83
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33; Conservative
 collagen alpha 1(VIII) chain;
iled coil; extracellular matri;
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Pred. No. 0.0041
1; Mismatches 1;
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complement Clq of
x; glycoprotein;
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A; Molecule type: mRNA
A; Residues: 580-596, 598-620, 'R', 622-813; 835-884 <KIM>
R; Residues: 580-596, 598-620, 'R', 622-813; 835-884 <KIM>
R; Muragaki, Y.; Nishimura, I.; Henney, A.; Ninomiya, Y.;

proc. Natl. Acad. Sci. U.S.A. 87, 2400-2404, 1990

A; Title: The alpha1(IX) collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen general general
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A; Residues: 1-253,'V',255-815;835-884 <NIN>
R; Kimura, T; Mattei, M.G.; Stevens, J.W.; Goldring, M.B.; Ni
Eur. J. Biochem. 179, 71-78, 1989
Eur. J. Biochem. 179, 71-78, 1989
A; Title: Molecular cloning of rat and human type IX collagen
A; Reference number: S02140; MUID:89137096; PMID:2465149
A; Accession: S02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-recervance, R;Ninomiya, Y.; Gastagnola, P.; Gerecke, L., maguchi, N.; Olsen, B.R. in Extracellular Matrix Genes, Sandell L.J. in Extracellular Matrix Genes, of collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 13-Jan-1995 #sequence revision 10-Feb-1995 #text change 20-Sep-1999 C;Accession: S13580; S23295; S02140; C35980; S21087; S74294 R;Muragaki, Y.; Kimura, T.; Ninomiya, Y.; Olsen, B.R. Eur. J. Blochem. 192, 703-708, 1990 A;Title: The complete primary structure of two distinct forms of human alpha A;Reference number: S13580; MUID:91006164; PMID:2209617 A;Accession: S13580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(IX) chain precursor, long W;Alternate names: procollagen alpha 1(IX) C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence revision 10-FC;Accession: $13580; $23295; $02140; $23588
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A; Residues: 1-931 < MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALLLLMSLNLVHG-----VFY---TERYQTFTG-IKGPPSNTKTQFFIPYAIKGKGVSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKPGLPGLKGQRGPVGLPGSPGAKGEQGPAGHPGEAGLPGPSGNMGPQGPKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCWRRRAKPSESRHP----GPGSFGRGGSLGLGGGGGGMGPREAEPGELGIA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPGERGLPG-----PQGPTGPPGPPGVGKRGENGLPGQPGLKGD-----QGVPGERGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGKPGL-----PGLPGKQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEQGIPGPPGPAGPRGHPGPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RPPGP-----HSSPNYEFYKLYLVG------GAQGR-RCEAPPAPNLLLT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LRG-GGAADPPFCPHYEKVSGDYGHPVYIVQDGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AGPSGPQGPPGEQGPEGIGKPGAPGIPGQPGIPGMKGQPGAPGTAGLPGAPGF
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splice form - human
chain, long splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Boyd C.D., eds., pp.79-114, Academic with short triple-helical domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 674; .01;
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                                                                                                                                                                                                                                                                                                                                                                                                M.B.; Ninomiya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 158;
                                         different transcripts in
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                                                                                                              Olsen,
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                                                                                                                                                                                                                                                                                                                                                                                                    Y.; Olsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LuValle,
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A;Gene: GDB:COL9A1

A;Gene: GDB:COL9A1

A;Cross-references: GDB:119794; OMIM:120210

A;Map position: 6q12-6q14

A;Introns: 5/2; 232/3; 260/3; 267/3

C;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(C;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(C;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(C;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) produced with type IX collagen alpha 1(IX) chain, predicted collagen alpha 1(IX) chain, long splice form #status predicted cMAT>

F;24-931/Product: collagen alpha 1(IX) chain, long splice form #status predicted cMAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-931/Product: collagen alpha 1(IX) chain, long splice form #stat
F;24-268/Domain: non-collagenous NC4 #status predicted <NC4>
F;269-405/Domain: collagenous COL3 #status predicted <COL3>
F;406-417/Domain: non-collagenous NC3 #status predicted <NC3>
F;418-756/Domain: collagenous COL2 #status predicted <NC2>
F;418-756/Domain: collagenous NC2 #status predicted <NC2>
F;757-786/Domain: non-collagenous NC1 #status predicted <NC2>
F;787-901/Domain: non-collagenous NC1 #status predicted <NC1>
F;902-931/Domain: non-collagenous NC1 #status predicted <NC1>
F;1071/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 405-417 < DIA>
C; Comment: Prolines and l;
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A;Molecule type: DNA
A;Residues: 1-4;233-267 <MUR2>
A;Cross-references: EMBL:M32135
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A;Accession: S74294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Diab, M.; Wu, J.J.; Eyre, Biochem. J. 314, 327-332, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comment: Prolines and lysines at and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: Collagen type IX from human cartilage: a structural profile of Reference number: S64673; MUID:96195147; PMID:8660302
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Cross-references: EMBL:M32135
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Residues: 1-4;
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                                                DYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLGSPGLPGLPGPPGLP
                                                                                                    VAGEKGSTGAPGKPGQMGNSGKPGQQGPPGEVGPRGPQGLPGSRGELGPVGSPGLPGKLG
                                                                                                                                                       LGGGGGMGPREAEPGELGIALRGG----
                                                                                                                                                                                                        GLPGPKGDTG-----LPGVDGRDGIPGMPGTKGEPGKPGPPGDAGLQGLPGVPGIPGAKG
                                                                                                                                                                                                                                                      SMPAVAGAAGGLALLILGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLG 276
                                                                                                                                                                                                                                                                                                         GLRGITGLVGDKGEKGARGLDGEPGPQGLPGAPGDQGQRGPPGEAGPKGDRGAEGARGIP 528
                                                                                                                                                                                                                                                                                                                                                          PRKPVSEMPMERDRGAAHSL--EPGKENLPGDPTSNAT-----SRGAEGPLPPP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPNACPPGRSGYPG-----LPGMRGHKGAKGEIGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPRARPPGPHSSPNYEFYKLYLVG-----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
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                                                                                                                                                       GAADPPFCPHYEKVSG 316
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A;Nolecule type: protein
A;Nolecule type: protein
A;Residues: 1-95;'X',97-107,'X',109-191,'X',193-260,'X',262-278,'X',280-572,
A;Note: we have shown the unidentified residues as Lys forming glycosylated
A;Mann, K.; Gaill, F.; Timpl, R.
submitted to the Protein Sequence Database, July 1992
A;Description: Amino acid_sequence and cell adhesion activity of a fibril-fo
                                                                                                                                                                                                                                                                            collagen alpha chain - tube worm (Riftia pachyptila) (fragment) (Species: Riftia pachyptila (Species: Riftia pachyptila (Species: Riftia pachyptila (Spate: 22-Nov-1993 #sequence revision 09-Mar-1996 #text_change (Spate: 22-Nov-1993 #sequence revision 09-Mar-1996 #text_change (Spate: Selection: S28774; S22915; S17581 R. R. R. R. R. R. Gaill, F.; Timpl, R. Eur. J. Biochem. 210, 839-847, 1992 A. Title: Amino-acid sequence and cell-adhesion activity of a fik A. Reference number: S28774; MUID:93130909; PMID:1483468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Modecule type: protein
A;Residues: 1-90;91-254;255-304;305-374;375-438 <GAI>
C;Superfamily: unassigned collagens
C;Keywords: coiled coil; extracellular matrix; glycoprotein
                                                                                        A;Description: Amino acid sequence A;Reference number: S22915
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R;Gaill, F; Mann, K.; Wiedemann, H.; Engel, J.; Timpl, J. Mol. Biol. 246, 284-294, 1995
A;Molecule type: protein
A;Residues: 1-95, 'X', 97-107, 'X', 109-191, 'X', 193-260, 'X', 262-278, 'X', 280-572, 'X', 574-611,
A;Note: 903-proline modified to 4-hydroxyproline was also found
                                                                    A;Accession: S22915
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;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 07-May-1999
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Pred. No. 0.0
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C;Keywords: cell binding; coiled coil; extracellular matrix; glycoprotein; homotrimer; h F;1-12/Domain: amino-terminal telopeptide (fragment) cNTE>
F;1-12/Domain: collagenous #status experimental cCOL>
F;1024-1027/Domain: carboxyl-terminal telopeptide (fragment) cTE>
F;1024-1027/Domain: carboxyl-terminal cTE>
F;1
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C;Superfamily: unassigned collagens
C;Superdamily: unassigned colled coil;
C;Keywords: cell binding; colled coil;
F;1-12/Domain: amino-terminal telopepti
F;1-12/Domain: collagenous #status 6
                                                                                 collagen alpha-4 chain precursor - sea urchin (Strongylocentrotus N,Alternate names: collagen alpha 2 (IV) chain homolog C,Species: Strongylocentrotus gurpuratus (purple urchin) G,Date: 07-Uul-1995 #sequence_revision 07-Uul-1995 #text_change 13 C,Accession: A54121; S44317 R,Exposito, J.Y.; Suzuki, H.; Geourjon, C.; Garrone, R.; Solursh, J. Sizuki, H.; Geourjon, C.; Garrone, R.; Solursh, J. Biol. Chem. 269, 13167-13171, 1994
A,Tible: Identification of a cell lineage-specific gene coding for A,Reference number: A54121; MUID:94230414; PMID:8175744
A,Faccession: A54121
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 8-45;525-545,'X',547-566,'X',568-572,'X',574-611,'X',613-618;'X',811-882
C;Comment: Prolines and lysines at the third position of the tripeptide repeating uni
h 3- and 4-hydroxylated in the X-position. Lysines are 5-hydroxylated and subsequent
C;Complex: homotrimer
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A;Title: Molecular characterization of cuticle and interstitial collagens A;Reference number: S17581; MUID:92015209; FMID:1920405
               A;Molecule type: mRNA
A;Residues: 1-1747 <EXP>
A;Cross-references: EMBL:X76730;
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Pred. No. 0.01:
4; Mismatches
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                    PIDN:CAA54146.1; PID:g483607
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A; Accession: S23779
A; Status: preliminary
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C;Superfamily:
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C;Species: Mus musculus (house mouse)
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                                                                                                                                            TSDGT----
                                                                                                                                                                                        LRGEQGPRGEPGPRGPPGP-
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Pred. No. 0.04;
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A;Molecule type: DNA, A;Rosidues: 1-743 kMR, A;Residues: 1-743 kMR, A;Residues: 1-743 kMR, A;Residues: 1-743 kMR, A;Cross-references: EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g1359953 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology cC1Q, F;616-742/Domain: complement C1q carboxyl-terminal homology cC1Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text C;Accession: $23779 R;Muragaki, Y: Shiota, C:; Inoue, M.; Ooshima, A.; Olse Bur. J. Biochem. 207, 895-902, 1992
A;Title: Alpha-1(VIII)-collagen gene transcripts encode A;Reference number: $23779; MUID:92362626; PMID:1499564
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                                                                                                                                                                                                                                                                                                                                  QQVPHMPLGKDGLSMGKEMPHMQYGKEYPYLPQYMKEIPPVPRMGKEVVPKKGKEVPLAS
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GPPGPHGLPGIGKPGGPGLPGQPGAKG-ERGPKGPPGPPGLQGPKGEKGFGMLGLPGLKG
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A;Cross-references: GB:X04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
A;Experimental source: rhabdomyosarcoma cell line
R;Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Biol. Chem. 260, 5533-5541, 1985
A;Title: Partial covalent structure of the human alpha 2 type V collagen cha.
A;Reference number: 155239; MUID:85182703; PMID:2985598
A;Accession: 155239; MUID:85182703; PMID:2985598
A;Ccession: 155239; MUID:85182703; PMID:2985598
A;Ccession: 155239; MUID:8182703; PMID:2985598
A;Ccession: 155239; MUID:8182703; PMID:3985807.1; PID:g180428
A;Ccess-references: GB:M10956; NID:g180427; PIDN:AAA52007.1; PID:g180428
A;Ccess-references: GB:M10956; NID:g180427; PIDN:AAA5200
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A;Residues: 1-32 <GRE>
A;Cross-references: GB:M58529; NID:g180834; PIDN:AAC41699.1; PID:g553235
A;Cross-references: GB:M58529; NID:g180834; PIDN:AAC41699.1; PID:g553235
R;Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.;
Eur. J. Biochem. 221, 987-995, 1994
A;Title: Diversity in the processing events at the N-terminus of type-V collagen.
A;Reference number: S43642; MUID:94237164; PMID:8181482
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A;Cross-references: GB:U04478; NID:g179697; PIDN:AAA51859.1;
A;Cross-references: placenta
A;Experimental source: placenta
R;Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gene Expr. 1, 29-39, 1991
A;Title: Homology between alpha2(V) and alpha1(III) collagen
A;Reference number: A54555; MUID:92314691; PMID:1820205
A;Accession: A54555
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C;Date: 31-Uul-1989 #sequence revision 28-Jul-1995 #text change 31-Dec-2000
C;Date: 31-Uul-1989 #sequence revision 28-Jul-1995 #text change 31-Dec-2000
C;Accession: A3147; A54555; S43643; A25874; I55239; I59025; A25374; A30017
C;Mcocbury, D.; Benson-Chanda, V.; Ramirez, F.
J. Biol. Chem. 264, 2735-2738, 1389
A;Molecule type: protein
A;Residues: 288-291,'P',293-294,'X',296-297;606,'X',608-617 <MOR>
A;Residues: 288-291,'P',293-294, 'X',296-297;606,'X',608-617 <MOR>
R;Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
Nucleic Acids Res. 15, 181-198, 1987
Nucleic Acids Res. 15, 181-198, 1987
A;Title: The pro alpha 2(V) collagen gene is evolutionarily related A;Reference number: A25874; MUID:87146331; PMID:3029669
A;Accession: A25874
                                                                                                                                                                                                                          A;Accession: I59025
A;Status: translate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA; DNA
A; Residues: 398-1496 <WEI>
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A; Residues: 1-463 < WOX
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                                                                                                                                                                                                                          Status: translated from GB/EMBL/DDBJ
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F;03-505/Region: cell attachment (R-G-D) motif
F;941-943/Region: cell attachment (R-G-D) motif
F;941-943/Region: cell attachment (R-G-D) motif
F;1064-1066/Region: cell attachment (R-G-D) motif
F;1064-1066/Region: cell attachment (R-G-D) motif
F;1067-1069/Region: cell attachment (R-G-D) motif
F;1097-1099/Region: cell attachment (R-G-D) motif
F;1097-1099/Region: cell attachment (R-G-D) motif
F;1133-1135/Region: cell attachment (R-G-D) motif
F;1251-1250/Region: cell attachment (R-G-D) motif
F;1
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A;Residues: 1449-1463,'E',1465-1495,'A' <TSI>
A;Residues: 1449-1463,'E',1465-1495,'A' <TSI>
A;Cross-references: GB:J03051; NID:g179695; PIDN:AAA51858.1; PID:g179696
A;Note: the authors translated the codon GAA for residue 1460 as Gln, and GAG for C;Comment: Prolines and lysines at the third position of the tripeptide repeating are 5-hydroxylated and subsequently O-glycosylated.
C;Comment: The amino-terminal propeptide domain appears not to be completely C;Genetics:
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A;Residues: 1227-1417,'T',1419-1437,'S',1439-1496 <MYE>
A;Residues: 1227-1417,'T',1419-1437,'S',1439-1496 <MYE>
A;Cross-references: GB:M11718; NID:g180912; PIDN:AAA52058.1; PID:g180913
A;Experimental source: normal fibroblasts
R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.;
Genomics 3, 275-277, 1988
A;Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL
A;Reference number: A30017; MUID:89138450; PMID:3224983
A;Accession: A30017
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A;Map position: 2q31-2q31
A;Introns: 33/1; 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 1448/C;Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV), a alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among the ength, is formed with desmosine cross-links made from lysine and allysine residues C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A25374; MUID:85289337; PMID:2411731 , A;Accession: A25374
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                                                                              Similarity
                                                                              7.7%; Score 142.5; DB 29.1%; Pred. No. 0.037;
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                                                                                                                                                    DB 1;
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76;
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               43;
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169 QSPRG--GAV-PRKPVSEMPMERDRGAAHSLEPGKENLPG------DPTSNATSRGAE 217

PGSDGLPGPKGAQGERGPVGSSGPKGSQ 554

RGPRGDPGTLGPPGPVGERGAPGNRGF---

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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-.
E;Accession: 51.5435; MUID: 91231001; PMID: 2029894
A;Accession: S15435; MUID: 91231001; PMID: 2029894
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S15425
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C;Species: Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-744 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology 1. -20/Domain: signal sequence #status predicted <SIG> ;21-744/product; collagen alpha 1(VIII) chain #status predicted <VAT> ;21-11/Region: amino-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;572-744/Region:
;617-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;118-571/Region: interrupted helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GDB:128104; OMIM:120251
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                                                                                                                                                                                           LGLGG-GGGMGPREAEPGELGIALRGGGAADP--PFCPHYEKVSGDYGHPVYIVQDGP--
                                                                                                                                                                                                                                                         VAGAGGAMCWRRRRAKPSESRHPG----
                                                                                                                                                                                                                                                                                                                                                                                    HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERGEQGPP 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMGLPGPKGSNGDPGKPGEAG----NPGVPGQRGAPGKDGKVGPYGPP---
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                                                                                                EGGIVGPQGPP
                                                                                                                                                            RGMGGVPGALGPR-GEKGPIGSPGIGGSPGEPGLPGIP-
                                                                                                                                                                                                                                                                                      ----PGMHGL-PGPVGLPGVGKPGVTGFPGPQGPLGKPGAPGEPGRQGPIGVPGVQGPPG
                                                                                                                                                                                                                                                                                                                      ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL----G
                                                                                                                              -----PQSPP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 23.9
73; Conservative
2(VI) chain precursor musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carboxyl-terminal nonhelical
complement Clq carboxyl-terminal homology <ClQ;</pre>
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23.5%;
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                                                                                                                                                                                                                         KPGQDGIPGQPGFPGGKGEQGLPGLPGAPGLPGIGKPGFPGPKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 142; DB 2
Pred. No. 0.019;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                      ------LRGPKGDKGFGMPGAPGVKGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN: CAA40748.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 744;
                                                                                                                                                              -GPMGPPGAIGFPGPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 126;
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                                   FSY 527
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A;Tile: Structure of cDNAs encoding the triple-helical domain of murine alpha-2(VI) corate oligonucleotides for generation of novel cDNA clones.

A;Reference number: $13745; MUID:91226374; PMID:1709252

A;Accession: $13745

A;Accession: $13745

A;Accession: $13745

A;Accession: $13745

A;Accession: $13745

A;Accession: $13745

A;Corse-references: $1360-294,'L',296-600 <CON>
A;Corse-references: $26:L06343; NID:912671; PIDN:AAA37441.1; PID:912672

A;Corse-references: $28:L06343; NID:912672; PIDN:AAA37441.1; PI
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A;Cross-references: EMBD:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
R;Ibrahimi, A.; Bertrand, B.; Bardon, S.; Amri, E.Z.; Grimaldi, P.; Ailha Biochem. U. 289, 141-147, 1993
A;Title: Cloning of alpha2 chain of type VI collagen and expression durir A;Reference number: S28808; MUID:93143659; PMID:8380980
A;Accession: S28808
A;Molecule type: mRNA
A;Residues: 266-1029 (IB2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X62332; R;Constantinou, C.D.; Jimenez, S Matrix 11, 1-9, 1991
GDRGLPGPRGPQ-GALGEPGKQGSRGDP
                                                                                                                              GGGGM-GPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP--PN
                                                                                                                                                                                                                                                                                                                                                                                                 LALLLLGVAGAGGAMCWRRRRAKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYPGEAGSPGERGDQGAKGDSGRPGRRGPPGDP-GDKGSKGYQGNNGAPGSPGVKGGKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VSEMPMER-DRGA-AHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGEF-----GSDG-RKGAPGLAGKNG---TDGQKGKLGRIGPPGCKGDPGSRGPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGPHGPKGYRGQK-----GAKGNMGE-PGEPGQKGRQGDPGIEGPIGFPGPKGVPGFKGE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
                                                                                                                                                                                                                                                            Similarity
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ilarity 29.7%;
Conservative 1
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Pred. No. 0.027;
5; Mismatches 125; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                        -SESRHPGP----GSFGRGGSLGLG
              GDAGPRGDSGQPGPKGDPGRPG
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A;Reference number: S16366
A;Accession: S16366
A;Molecule type: mRNA
A;Residues: 1-1763 <JBI>
A;Cross-references: GB:M67
C;Genetics:
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collagen alpha 1(III) chain precursor - human N;Alternate names: procollagen alpha 1(III) chain C;Species: Homo sapiens (man) C;Pate: 24-Apr-1984 #sequence revision 01-Sep-1991 C;Accession: S05272; S04642; PE0011; S01726; S0468 submitted to the EMBL Data Library, February 1989 A;Reference number: S05272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 2(IV) chain precursor - pig roundworm ()Species: Ascaris suum (pig roundworm)
C;Date: 04-Dec-192 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
C;Accession: S16366
R;Pettlitt, J.; Kingston, I.B.
J. Biol. Chem. 266, 16149-16156, 1991
A;Title: The complete primary structure of a nematode alpha-2(IV) collagen
A;Reference number: S16366; MUID:91340766; PMID:1714907
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                                                                                 ;1530-1763/Domain: carboxyl-terminal nonhelical, NCI #status predicted ;1530-1638/Domain: repeat NCI #status predicted <NCI1> ;1530-1638/Domain: repeat NCI #status predicted <NCI1> ;1639-1763/Domain: repeat NCI #status predicted <NCI2> ;1639-1763/Domain: specified specified specified ;134,394,41,536,539/Disulfide bonds: #status predicted ;126/Binding site: carbohydrate (Asn) (covalent) #status predicted ;1593-1599,1702-1709/Disulfide bonds: #status predicted
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPP--GPQGIK-GDRGIIGVPGFPGNDGANGRPGEPGPPGAPGWDGCNGTDGAPG----V 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EF----SDGPP-GPPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRPGLPGPPGF---KGDRGLDGLPGVPGLPGQKGEAGFPGRDGAKGARGPPGPPG----GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG--GAADPPFCPHYEKVSG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMKGEKGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQAGPRGPPGBAGPPGNPGIGSIGPKGDPGEQGPRGPQGPPGPVPSTGAKGTIIGPEGAP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQS-PRG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQIGDRLDLLCPRARP--PGPHSSPNYEFYKLYLVGGAQGRRCEA--PPAPNLLLTCDRP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPPHSGPGGVRVGALLLLGVLGL----VSGLSLEP----VYWNSANKRFQAEGGYVLY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P----GLPGPPGMPGFPGPPGVPGMKGEPAIGYAGAPGEKGDAGMPGMPGL----- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GEAGPRGFPGTPGVAGQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RDGFPGEKG----DRG----DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LPGMKGEKGLSGPAGPRGKE 308
                                                                                                              #text_change 21-Ji
7; A90399; A94562;
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                                                                                                                      S59511;
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A;Residues: 'V',107 L-14
A;Experimental source: liver
A;Experimental source: Siver street on to A90399
A;Note: author submitted corrections to A90399
A;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester,
R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester,
Am. J. Hum. Genet. 53, 62-70, 1993
Am. J. harantal somatic and germ-line mosaicism for (
Biochem. J. 311, 939-943, 1995

A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation
A;Reference number: S59511; MUID:96067614; PMID:7487954
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R;Toman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A;Title: Nucleotide sequence of a cDNA coding for the amino-terminal
A;Reference number: S01726; MUID:88303360; PMID:3405773
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A;Note: the complete sequence is not shown
R;Benson-Chanda, V; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
Gene 78, 25-265, 1989
A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen
A;Reference number: PE0011; MUID:89378752; PMID:2777083
                                                                                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 186-194 <MIL>
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Nucleic Acids Res. 17, 6742, 1989
A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) A;Reference number: S04887; MUID:89386015; PMID:2780304
A;Accession: S04887
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A;Cross-references: EMBL:X14420, NID:g30057; PIDN:CAA32583.1; PIR;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Biochem. J. 260, 509-516, 1989
                                                                                                A;Cross-references: GB:S62925; NID:g386425; R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Biochem. J. 311, 939-943, 1995
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A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398
A;Experimental source: liver
A;Experimental source: liver
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A;Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634
A;Cross-references: EMBL:X15332; NID:g59545; PIDN:CAA33387.1; PID:g930045
A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotid
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A;Status: prelimina
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A,Residuss: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398
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A;Reference number: A94562
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A;Residues: 1-170 <TO
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A; Residues: 1-176 <BEN>
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A; Residues: 1-1196 < ALA>
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iochemistry 16, 1158-1164, 1977
                                                                                                                                                                                                                                                                                                                                                                                                Reference number: I51868; MUID:93304430; PMID:8317500; Accession: I51868; Reference number: I51868; Reference number: I51868; Reference number: Reference nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide; Reference number: A90399; MUID:77134724; PMID:557335
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B.
                                                                                                                                             PIDN:AAD13937.1; PID:g4261637 Bateman, J.F.
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A;Molecule type: mRNA
A;Residues: 1065-1155,'P',1157-1466 <LOI>
A;Residues: 1065-1155,'P',1157-1466 <LOI>
A;Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
A;Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
A;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolsto:
Biochemistry 25, 1408-1413, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA;
A;Residues: 950-1018, 'Y',1020-1183,'S',1185-1466 <MAN>
A;Residues: 950-1018, 'Y',1020-1183,'S',1185-1466 <MAN>
A;Residues: 950-1018, 'Y',1020-1183, 'S',1185-1466 <MAN>
A;Coss-references: BMBL:X06700; NID:g30053; PIDN:CAA29886.1;
R;Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
Biochemistry 20, 2
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A;Residues: 537-605 <LEE>
A;Residues: 537-605 <LEE>
A;Cross-references: GB.M59312; NID:g180815; PIDN:AAA52041.1;
A;Cross-references: GB.M59312; NID:g180815; PIDN:AAA52041.1;
R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A;Title: Covalent structure of collagen: amino acid sequence
A;Reference number: A90438; MUID:80198282; PMID:6246925
A;Accession: A90438
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A;Residues: 399-675,'N',677-727 <SEY3>
A;Residues: 399-675,'N',677-727 <SEY3>
A;Resperimental source: liver
R;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.;
J Biol. Chem. 266, 5256-5259, 1991
A;Title: G to T transversion at position +5 of a splice
A;Reference number: I55349, MUID:91161621; PMID:1672129
A;Accession: I55349
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A;Residues: 861-1015 <COL>
A;Residues: 861-1015 <COL>
A;Residues: 861-1015 <COL>
A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PIA;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos R;Mankoo, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
Nucleic Acids Res. 16, 2337, 1988
A;Title: Human pro alphal(III) collagen: cDNA sequence for the 3' end.
A;Reference number: S02119; MUID:88189827; PMID:3357782
A;Accession: S02119
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A;Residues: 728-895, 'A',897-964 <SEY4>
A;Residues: 728-895, 'A',897-964 <SEY4>
A;Reperimental source: liver
R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ran
J. Biol. Chem. 265, 17070-17077, 1990
A;Title: A base substitution at a splice site in the COL3A1
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416 R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C. Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
                                                                                                                          A; Molecule type: mRNA
A; Residues: 1161-1200 < MIS>
                                                                                                                                                                                                                                                     Biochemistry 25, 1408-1413, 1986
A;Title: Human type III collagen gene expression is coordinately
A;Reference number: I52393; MUID:86187804; PMID:3754462
A;Accession: I52393
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;Title: Covalent structure of collagen: amino acid sequence;Reference number: A90414; MUID:79000343; PMID:687591
;Accession: A90414
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A;Genes iods: Odds: Idds: 
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A;Title: Isolation of cDNA and genomic clones encoding human A;Reference number: A92516; MUID:85157600; PMID:2579949
A;Accession: A92516
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A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Residues: 1176-1240,'V',1242-1356,'B:M10793; GB:M10794; GB:M10795;
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795;
A;Experimental source: liver
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A; Residues: 1165-1196 < EMA>
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                                                             MPGPRGSPGPQGVKGESGKPGANGLSGERGPPGPQGLPGLAGTAGEPGRDGNPGSDGLPG
                                                                                                                                 KPSESRHPGP----GSFGRGGSLGLGG-GGGMGP--
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llarity 27.6%;
Conservative 1:
GAADPPFCPHYEKVSGDYGHPVYIVQDGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 141.5; DB
Pred. No. 0.042;
3; Mismatches
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PMID:3858826
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                                                                                                                                                                                                                                                                   -ALLLIGVAGAGGAMCWRRRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1466;
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Ramirez, F.
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J. Biol. Chem. 264, 16022-16029, 1989

A.Title: The cloning and sequencing of alphal(VIII) collagen cDNAs demonstrated comains similar to those of type x collagen.

A;Reference number: A34246; MUID:89380199; PMID:2476437

A;Recession: A34246

A;Molecule type: mRNA

A;Residues: 1-744 < YAM>

A;Residues: 1-744 < YAM>

A;Cross-references: GB:JO5042; NID:g164895; PIDN:AAA31204.1; PID:g164896

C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxy1-terminal

F;12-20/Domain: signal sequence #status predicted <SUG>
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted

F;21-117/Region: amino-terminal nonhelical

F;118-571/Region: interrupted helical

F;572-744/Region: carboxy1-terminal homology <C1Q>
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A;Reference number: 2
A;Accession: T32250
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:T15B
A;Map position: 5
A;Introns: 266/1
C;Superfamily: un
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C;Species: Ca
C;Date: 29-Oc
C;Accession:
R;Pauley, A.;
                                                                                                                                                                                                                                                                                                                   collagen alpha 1(VIII) chain precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: A34246
R;Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Nir J. Biol. Chem. 264, 16022-16029, 1989
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A34246
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R;Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, Septem
comparison. The sequence of C. elegans
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A; Residues: 1-319 < PAU>
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Best Local S
Matches 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VGALLLLGVLGLVSGLSL-----EPVYWNSANKRFQAEGG----YVLYPQIGDRLDLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRARPPGPHSSPNYEFYKLYLVG------GAQGRRCEA-PPAPNLLLTCDRPDLDL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSASTLVTVASAASGIAIVVCVFTVGMIFNDINSFYDEKIGELKEFKGYEQIA--WQAMI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein T15B7.3 - Ca
Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                      P.D.; van der Rest, M.; Ninomiya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 141; DB 2; I
25.6%; Pred. No. 0.0088;
ative 27; Mismatches 111;
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                                                                                                                                         carboxyl-terminal
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R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, maguchi, N.; Olsen, B.R. in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. A;Title: The molecular biology of collagens with short triple-helic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen alpha 1(VIII) chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A;Residues: 1-744 <NIN>
A;Residues: 1-744 <NIN>
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
F;617-743/Domain: complement Clq carboxyl-terminal homology <ClQ>
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A;Accession: S23298
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Best Local
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Best Local Similarity
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 PP---FCPHYEKVSGDYGH---
                                                                        KPSESRHPG-PGSFGRGGSLGL----GGGGGMGPR-----EAEPGELGIALRGG--GAAD 304
                                                                                                          KGEQGLPGLPGPPGLPGVGKPGPPGPKGD-----RG1GGVPGALGPRGEKGPVGAPGMGG
                                                                                                                                                                                                                                                                                                                          PPGPHGLPG-----IGKPGGPGLPGQPGAKGDRGPKGPPGP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPGPHGLPG-----IGKPGGPGLPGQPGAKGDRGPKGPPGP
                                    PPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPGPKGEPGLQGFPGKPGFLGEVG
                                                                                                                                           ATSRGAEGPLPPPSMPAVA-----GAAGGLALLLLGVAGAGGAMCWRRRR------A
                                                                                                                                                                             xpgvTgFpGpQgpLgkpGppGepGpQgpIGvpGvpGqppGLpGvGkpGQDGIPGQpGFpGG
                                                                                                                                                                                                                                                   -----PGLQGPK------GEKGFGMPGLPGLKGPPGMHGPPGPVGLPGVG
                                                                                                                                                                                                                                                                                    IKFQEYSPNLWGHEFRSHHDYYIIATSDGTR----EGLESLQG--GVCLTRGMKVLLRVG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPSESRHPG-PGSFGRGGSLGL----GGGGGMGPR----EAEPGELGIALRGG--GAAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGPHSSPNYEFYKLYLVG------GAQG-RRCEAPPAPNLLLTCDRPDLDLRFT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGIRGLPGPIGPKGEAGHKGLPGLPGVPGLLGPKGEPGIPGDQGLQGPPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PP---FCPHYEKVSGDYGH-----PVYIVQDGPP-----QSPPNI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPGPKGEPGLQGFPGKPGFLGEVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPGVTGFPGPQGPLGKFGPPGBPGPQGPIGVPGVQGPPGLPGVGKPGQDGIPGQPGFPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                83;
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                             -----SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP--TSN
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                                                                                                                                                                                                                                                                                                                                                                                                                7.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 1
Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 141; DB 1
Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
 -PVYIVQDGPP-
                                                                                                                                                                                                                                                                                                                                                          -GAQG-RRCEAPPAPNLLLTCDRPDLDLRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Boyd C.D., eds., pp.79-114, Academic with short triple-helical domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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 -QSPPNI
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                                    447
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                                                                                                                                                                                                                                                                                                                                                                                                  19;
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C;Species: Car
C;Date: 15-Oct
C;Accession:
R;Latreille,
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A; Molecule type: DNA
A; Residues: 1-305 <LAT>
A; Cross-references: EMBL: U80444; PIDN: AAB37788.1; GSPDB: GN00019; CESP: F26B1.4
A; Cross-references: Strain Bristol N2; clone F26B1
                                                     A; Map position:
a.Introns: 27/3
                                                                                                                                                               A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-304 <WIL>
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A; Accession: T22482
                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z19569
                                                                                                                                                                                                                                                                                                hypothetical protein F52B11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-OCt-1999 #tesC;Date: 15-OCt-1999 #tesC;Accession: T22482
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A; Introns: 51/3; 77/1
C; Superfamily: unassi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: T30165
A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Latreille, P.; Wamsley, P.; Kramer, J. submitted to the EMBL Data Library, November 1996 A;Description: The sequence of C. elegans cosmid
                                                                                                                              A; Experimental source:
                                                                                                                                                A;Cross-references: EMBL:Z82268; PIDN:CAB05195.1; GSPDB:GN00022;
                                                                                                                                                                                                                                                                                R; Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: F26B1.4
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;Species: Caenorhabditis elegans
;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                     Superfamily:
                                                                                            Gene: CESP:F52B11.4
                                                                                                                Genetics:
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Best Local .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPHYEKVSGDYGHPVYIVQDGPPQSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPGLAGAPGDSGAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGEPGLPGPVGDPGFDGKPGNPGNNGVRVRRIPGPPGPRGAE-GDSGV--QGG-----PG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLRHDPGRCAQCPAGPMGPPGPRGPPGVPGITGAPG-----LDGIPGRHGTPGY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
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ilarity 25.8%;
Conservative 2
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                                   collagens
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 Score 140;
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2
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 Length 304;
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                                                                                                                                                    CESP: F52B11.4
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Query Match

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A; Molecule type: DNA
A; Residues: 561-647; 'G', 649-666 <AP2>
A; Residues: 561-647; 'G', 649-666 <AP2>
A; Residues: 561-647; 'G', 649-666 <AP2>
A; Cross references: EMBL:XS8879; NID:g30013; PIDN:CAA41686.1; PID:g30014
R; Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E Biochem. J. 280, 617-623, 1991
Biochem. J. 280, 617-623, 1991
A; Title: The human collagen X gene. Complete primary translated sequence and A; Reference number: S18249; MUID:92109659; PMID:1764025
A; A; Accession: S18249
A; A; Accession: S18249
A; Molecule type: DNA
A; Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A; Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30094; PIDN:CAA42933.1; PID:g30094; PIDN:CAA4003.1; PIDN:CAA4003.1; PIDN:CAA4003.
A;Molecule type: mRNA, A;Residues: 547-656 <RE2>
A;Residues: 547-656 <RE2>
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014) R;Natlis; G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans Am. J. Hum. Genet. 54, 169-178, 1994
A;Title: Amino acid substitutions of conserved residues in the carboxyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 'TIPPYGWVGWVCLL', 52-680 <APT>
A;Residues: 'TIPPYGWVGWVCLL', 52-680 <APT>
A;Cross-references: EMBL:X65120; NID:923129
A;Note: the initial difference is probably due to translation
R;Note: S; Mattei, M.G.; Olsen, B.R.
R;Apte, S; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
FEBS Lett. 282, 393-396, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text change 22-Jun-1999
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R;Reichenberger, E; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.;
FEBS Lett 311, 305-310, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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A;Title: Cloning of human alpha-1(X) collagen DNA and localization A;Reference number: S15826; MUID:91243838; PMID:2037056
A;Accession: S15826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A;Reference number: S30085 A;Accession: S30086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genomic organization and full-length cDNA sequence of human A;Reference number: S26396; MUID:93012005; PMID:1397333
A;Accession: S26396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.0099;
5; Mismatches 87;
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        the carboxyl-terminal domain
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                                                                                     G.; Grant,
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be important for skeletogenesis
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
C;Superfamily: collagen alpha 1(VIII) chain; glycoprotein; homotrimer; hydroxylysine;
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine;
F;11-18/Domain: signal sequence #status predicted <SIG>
F;11-18/Domain: signal sequence #status predicted <MAT>
F;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Coss-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
A;Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
A;Note: a second mutant sequence with 614-Pro is also described
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
                                                                                                                                                                                                             C;Accession: B44984
R;Shamansky, L.M.; Pratt, D.; Boisvenue, R.J.; Cox, G.N. R;Shamansky, L.M.; Pratt, D.; Boisvenue, R.J.; Cox, G.N. Mol. Biochem. Parasitol. 37, 73-86, 1989
A;Title: Cuticle collagen genes of Haemonchus contortus A;Reference number: A44984; MUID:90136718; PMID:2615789
A;Accession: B44984
                                                                                                                                                                                                                                                                                                                                                            collagen -
C;Species:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasis C;Complex: type X collagen may be a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: I51870; MUID:94136476; PMID:8304336
A;Accession: I51870
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                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-210 <SHA>
A;Cross-references: GB:J04671; GB:J04670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: structural component of extracellular fibrous polymer
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                                                                                                                                                                                               Status: preliminary
                                                                                                                                                                                                                                                                                                                                  ollagen - nematode (Haemonchus contortus) (fragment)
;Species: Haemonchus contortus
;Jate: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change
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Best Local :
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    176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDP--TSNATSRGAEGPLPPPSMPAVAGAAG 233
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57; Conserv
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Pred. No. 0.023;
3; Mismatches
                                                           Score 139.5;
Pred. No. 0.
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                                                           .5; DB 2;
0.0072;
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A; Residues: 1-940 <TOT>
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JE0291
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                                                                                                                                                                                                                                                                               YIVQDGP
                                                                                                                                                                                                                                                                                                                          MGNSSGHRPHEGPGGGMGSGHRPHEGPGGSMG----
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collagen alpha 1(XI) chain - bovine (fragments)
(/Species: Bos primigenius taurus (cattle)
(/Species: Bos primigenius taurus (cattle)
(/Date: 22-Nov-1993 #sequence revision 23-Mar-1995 #text change 02-Jul-1998
(/Accession: S18251; C46662; Ā56978; S65884; D46662; E46662; F46662; G46662;
R,Brown, K.E.; Lawrence, R.; Sonenshein, G.E.
J. Biol. Chem. 266, 23268-23273, 1991
A,Title: Concerted modulation of alpha-1(XI) and alpha-2(V) collagen mRNAs ir
A,Reference number: S18251; MUID:92078200; PMID:1744123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: JE0291

R;Totaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Vale Biochem. Biophys. Res. Commun. 250, 555-557, 1998

A;Title: Cloning of a new gene (FB19) within HLA class I A;Reference number: JE0291; MUID:99003493; PMID:9784381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Y13247; NID:g2117158; PIDN:CAA73697.1; PID:g2117159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Homo sapiens (man)
;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 GLALLLLGVAGAGGAMCWRRRRAKPSESRHPG----PGSFGRGGSLGLGGGGGMGPREAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRGAEGPLPPPSMPAVAGAAGGLA--LLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRGGDPFWDGPGDPMRGGPMRGGPG-----PG----PGPYHRGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 139;
Pred. No. 0
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                                       collagen mRNAs in bovine
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J. Biol. Chem. 270, 18865-18870, 1995
A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins A;Reference number: A56978; MUID:95370194; PMID:7642541
A;Accession: A56978
A;Accession: A56978
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-229 <MUA>
R;Niyibizi, C; Eyre, D.R.
Eur. J. Biochem. 224, 943-950, 1994
A;Title: Structural characteristics of cross-linking sites in type V collagen of bone. C
A;Reference number: S48210; MUID:95010086; PMID:7925418
A;Accession: S55864
A;Molecule type: protein
A;Residues: 'X',273-298 <NIY>
C;Superfamily: collagen alpha 1 (V) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: hydroxyproline
F;211,223/Modified site: 4-hydroxyproline (Pro) #status experimental
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A24450
A24450
Collagen alpha 2(VIII) chain - bovine (fragment)
Collagen (VIII), Descemet's
N;Alternate names: 50K-A collagen (VIII), Descemet's
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1988 #sequence_revision 05-Apr-1995 #t
C;Accession: S12898; A24450
R;Mann, K.; Jander, R.; Korsching, E.; Kuehn, K.; Raufels
FEBS Lett. 273, 168-172, 1990
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R;Mayne, R.; Brewton, R.G.; Mayne, I
J. Biol. Chem. 268, 9381-9386, 1993
A;Title: Isolation and characterizal
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A;Molecule type: mRNA
A;Residues: 1-911 <BR
                                                                                                                                                                                               RESULT 47
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                                                                                                                                                                                                                                                              GPPGPLGPPGL
                                                                                                                                                                                                                                                                                                      GP--PQSPPNI 336
                                                                                                                                                                                                                                                                                                                                               FPGPPGPIGLQGLPG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LPGPAGPAGS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GHPGPPGPPGEQG-----LPGAAGKEGAKGDPGPQGVSGKDGP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                          -GSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 24.3%;
Conservative 1
                                                                                                                                                                                                                                                              990
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Pred. No. 0.043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                             Rauterberg,
                                                                                 #text_change
                                                                                                                                  membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PGSFGRG----
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                                                                                       03-May-1996
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A; Molecule type: protein
A; Residues: 1-469 < MAN>
R; Kapoor, R.; Bornstein, P.; S
Biochemistry 25, 3930-3937, 19
A; Title: Type VIII collagen fr
A; Reference number: A90507; MU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The primary structure of a triple-helical domain A; Reference number: $12898; MUID:91032171; PMID:2226849
                                                                                                                                                                                                                                                                                                                                                         ;Superfamily: collagen alpha 1(VIII) chain; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                        377
                                                                                                                   327
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433
                          301
                                                                                      273
                                                                                                                                               234
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                            GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                 PSGLA----GKPGLPG-----ERGLPGAHGPPGPTGPXGEPGFTGRPGGPGAAGALGQX
                                                                                                                                               --GLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP
                                                                                      GSLGI
                                                                                                                                                                                                                                      GLPGPQGPPGAXGEPGTRGPPGLI----GPTGYGMPGLPGPXGDRGPAGVPGLLGDRG--
                                                        GDLGLPGQPGLRGPSGIPGLQGPAGPIGPQGLPGLXGEPGLPGPPGEGKVGEPGVA----
                                                                                                                                                                           ---EPGEDGEPGEQGPQGLGGPPGLPGSAGLPGRRGVPGPXGETGPIGPPGVPGIRGDQG
                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                           7.5%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                   from bovine Descemet's membrane:
MUID:86296625; PMID:3527259
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sage,
                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                             Score 138.5;
Pred. No. 0.0
                                                                                                                                                                                                        PTSNAT-----SRGAEGPLPPPSMPAVAGAAG
                                                                                                                                                                                                                                                                                                Mismatches
459
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                                                                                                                                                                                                                                                                    RKPVSEMPMERDRGAA
                                                                                                                                                                                                                                                                                                                            Length
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                                                                                      EAEPGELGIALRGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 structural characterization
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                                                                                                                                               GSFGRG
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A;Status: preliminary; not compared with conceptual transla A;Molecule type: DNA A;Residues: 1-1419 <MET> A;Cross references: GB:M65161 A;Cross references: GB:M65161 R;Cheah, K.S.; Lau, B.T.; Au, P.K.; Tam, P.P. Development 111, 945-953, 1991 Development 111, 945-953, 1991 A;Title: Expression of the mouse alpha 1(II) collagen gene A;Reference number: A44885; MUID:91347939; PMID:1879363 A;Accession: A44885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence revision 28-May-1992 #text_change 13-Aug-1999
C;Accession: A41182; A44885
R;Metsacranta, M; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J;Biol. Chem. 266, 18862-18869, 1991
A;Title: Mouse type II collagen gene. Complete nucleotide sequence, exon stip. Reference number: A41182; MUID:91358489; PMID:1885613
A;Accession: A41182
                                                                                                                                                     A,Cross-references: GB:S63190; NID:g234368; PIDN:AAB19627.1; PID:g234369 A,NOte: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192) C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal C;Keywords: alternative splicing; colled coil; extracellular matrix; glycoprote F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-28 < CHE>
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                                                     Matches
                                                                            Query Match
Best Local &
  173 GGAVPRKPVSEMPMERDRGAAHSLEPGKENL-----PGD--PTSNATSRGAEGPLPPPS 224
                                                                              Similarity
                                                     Conservative
                                                                            7.5%;
                                                     13;
                                                                            Score 138.5;
Pred. No. 0.0
                                                     Mismatches
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                                                        Indels
                                                                                                     Length 1419;
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<FCC>
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ein; trim
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C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-J
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-J
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-J
C;Date: Mouse type I collagen gene. Complete nucleotide sequence,
A;Title: Mouse type II collagen gene. Complete nucleotide sequence,
                                                                                                                                             collagen alpha 2(XI) chain precursor - human (fragment)
N;Alternate names: procollagen alpha 2(XI) chain
N;Contains: proline/arginine-rich protein (PARP)
C;Species: Homo sapiens (man)
C;Date: 07-Uun-1990 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Accession: S34790; A32645
C;Accession: S34790; A32645
R;Zhidkova, N.I.; Brewton, R.G.; Mayne, R.
FEBS_lett. 326, 25-28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-1487 <MET>
A;Residues: 1-1487 <MET>
A;Residues: 1-1487 <MET>
A;Residues: 1-1487 <MET>
A;Cross-references: GB:M65161
C;Superfamily: collagen alpha 1(I) chain, fibrillar collagen carboxyl-terminal homology;
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
F;33-91/Domain: von Willebrand factor type C repeat homology <VWC>
F;33-91/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
A;Accession: S34790
A;Molecule type: mRNA
A;Residues: 1-663 <ZHI>
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A;Accession: B41182
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                                                                          A; Reference number: S34790; MUID: 93314796; PMID: 8325374
                                                                                                                        A; Title: Molecular cloning of PARP (proline/arginine-rich protein)
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Best Local S
Matches 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 SGFQGLFGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGANGEPGKAGEKGLAGAPGLRGLPGKDGETGAAGPPGPSGPAGERGEQGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGMGPREAEPGELGIA----LRG-----GGAADPPFCPHYEKVSGDYGHPVYIVQDGP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPGLPGARG-----LTGRPGDAGPQGKVGPSGAPGEDGRPGPPGPQGARGQPGVMGFPGP 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGPIGPPGERGAPGNRGF-----PGQDGLAGPKGAPGERGPSGLAGPKGANGDPGRPG 552
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Pred. No. 0.0
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                                                                                                                           human
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A; Description: structural component of extracellular fibrous polymer associated with ce A; Note: may play a role in controlling the lateral growth of collagen II fibrils C; Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology C; Keywords: coiled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol F;1-254/Domain: non-collagenous (fragment) #status predicted <NC3> F;1-187/Product: prolline/arginine-rich Pharp protein (fragment) #status predicted <NC3> F;365-342/Domain: non-collagenous #status predicted <NC3> F;366-342/Domain: non-collagenous #status predicted <NC2> F;367-342/Domain: non-collagenous #status predicted <NC2> F;367-342/Domain: non-collagenous #status predicted <NC2> F;367-343/Region: cell attachment (R-G-D) motif F;447-449/Region: cell attachment (R-G-D) motif F;1357-1380/Region: cell attachment (R-G-D) motif F;1357-1380/Region: carlboxyl-terminal nonhelical telopeptide F;3381-1546/Domain: carboxyl-terminal propeptide (fragment) #status predicted F;1381-1545/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #status fragment) H;1426/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #status fragment) R;1426/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #status fragment) R;1426/Domain: graphine (Lys) #status fragment) #status fragment) R;1426/Domaining site: carbohydrate (Lys) (covalent) #status predicted F;126/Modified site: 5-hydroxylysine (Lys) #status experimental F;942,1023,129/Binding site: carbohydrate (Lys) (covalent) #status experimental F;1427,1433,1450,1459/Disulfide bonds: interchain #status predicted F;1427,1433,1450,1459/Disulfide bonds: interchain #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 6p21.3-6p21.3
A;Introns: 1302/3; 1330/3; 1332/3; 1350/3; 1440/1; 1477/3
A;Introns: 1302/3; 1330/3; 1332/3; 1350/3; 1440/1; 1477/3
A;Note: the list of introns is incomplete
C;Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR:CG C;Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR:CGHUGC), initially linked by disulfide bonds among their carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA < RNA
A; Residues: 586-1546 < KIN's
A; Residues: 586-1546 < KIN's
A; Cross-references: GB:J04974; NID:g180714; PIDN:AAA52034.1; PID:g180715
A; Note: parts of this sequence were determined by protein sequencing
C; Comment: Prolines and lysines at the third position of the tripeptide:
ed and subsequently O-glycosylated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
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KGEKGVQGPPGHP---
                                                                      HYEK-VSGDYGHPVYIVQDGPP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSEGROGG----KGAK-----GDPGAIGAPGKTGPVGP-----AGPAGKPGPDGLR 1224
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                                                                                                                                                    -EQGEKGDRGLÞGÞQGSÞGQKGEMGIÞGASGÞIGÞ-GGÞÞGLÞGÞAGÞKGAKGATGÞGGÞ
                                                                                                                                                                                                                                                                                                    GLPGSVGQQGRPGATGQAGPPGPVGPPGLPGLRGDAGAKGEKGHPGLIGLIGPPG-----
                                                                                                                                                                                                                                                                                                                                                                              GDPTS-----NATSR-GAEGPLPPPSMPAVAGAAGGLALL----LLGVAGAGGAMCWR 252
                                                                                                                                                                                                                          RRRAKPSESRHPGP-GSFGRGGSLGL-GGGGGMGPREAEPGELGIA-LRGGGAADPPFCP
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---GPP 1353
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Pred. No. 0.072;
8; Mismatches
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Search completed: February 11, 2003, 12:06:08
Job time : 36.805 secs

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Result
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Listing first 50 summaries
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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
   25548876 residues
                   US-10-138-787-4
US-10-138-787-5
US-10-138-787-13
US-10-138-787-13
US-09-862-179A-17
US-09-864-761-48257
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US-09-925-297-639
US-09-862-179A-15
US-10-138-787-12
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Sequence 4, Appli
Sequence 2, Appli
Sequence 10, Appli
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Sequence 5, Appli
Sequence 13, Appl
Sequence 13, Appl
Sequence 48267, A
Sequence 48267, A
Sequence 619, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 10, Appl
Sequence 12, Appl
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ALIGNMENTS

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US-10-021-121-4
Sequence 4, Application US/10021121
Sequence 4, Application US/10021121
Sequence 4, Application US/10021121
Sequence 4, Application US/10021121
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W
APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATES: 0416 Cannel tech, Inc.
STREET: 1 DNA Way
COUNTRY: USA
ZIP: 94080
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
FILING DATE: 10-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOTCCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELEPOMMUNICATION INFORMATION:
TELEPONE: 650/25-8674
TELEPONE: 650/25-8674
TELEPONE: 650/95-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
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Sequence 3, Application US/10138787

| Sequence 3, Application US/10138787
| Patent No. US20020172984A1
| GENERAL INFORMATION:
| APPLICANT: Holland, Sacha
| APPLICANT: Mbamalu, Geraldine
| TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
| TITLE OF INVENTION: TYROSINE KINASES
| FILE OF INVENTION: TYROSINE KINASES
| FILE REFERENCE: 11757.23USMO
| CURRENT APPLICATION NUMBER: US/10/138,787
| CURRENT APPLICATION NUMBER: US/09/214,631
| PRIOR APPLICATION NUMBER: US/09/214,631
| PRIOR APPLICATION NUMBER: PCT/CA97/00473
| PRIOR APPLICATION NUMBER: PCT/CA97/00473
| PRIOR APPLICATION NUMBER: PCT/CA97/00473
| PRIOR FILING DATE: 1997-07-04
| PRIOR FILING DATE: 1996-07-05
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: US/021,272
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TYPE: Amino Acid
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TOPOLOGY: Linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4
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                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 340
TYPE: PRT
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                                                                                           MGPPHSGPGGVRVGALLLLGVLGIVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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                               LCERARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
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   LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
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Pred. No. 8.7e-126;
0; Mismatches 0;
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RESULT 3
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                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: Amino Acid
121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOrchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELEPHONE: 650/225-8674
TELEPHONE: 650/225-8674
                                                                                                                                                                                            1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear SEQ ID NO: 2:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genented
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TITLE OF INVENTION: A2-1 Neurotrophic Factor
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                                                                             LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
                                                                                                                                           MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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                                              LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
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                                                                                                                                                                                                                                             338;
                                                                                                                                                                                                                                                                  Similarity
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CITY: South San Francisco
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                                                                                                                                                                                                                                     99.5%; Score 1841; DB 12; ilarity 100.0%; Pred. No. 5.3e-125; Conservative 0; Mismatches 0;
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US-10-021-121-9
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Best Local Similarity
Matches 145; Conserv
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Patent No. US20020142444A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/021,121

FILING DATE: 06-Dec-2001

CLASSIFICATION NUMBER: US/08/635,130

PRIOR APPLICATION NUMBER: US/08/635,130

PRIOR APPLICATION NUMBER: US/08/635,130

FILING DATE: 19-Mar-1996

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1001

TELEPHONE: 650/225-8674

TELEPHONE: 650/225-8674
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TITLE OF INVENTION: A2-1 Neurotrophic Factor
                                                                                                                                                                      PGGVRVGALLLLGVLGLVSGL-----SLEPVYMNSANKRFQAEGGYVLYPQIGDRLDLL 61
                    PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                         CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
                                                                                           CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCSAPPAPNLLLITCDRPDLDLRFTIKFQEYS 121
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PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                                  PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
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TYPE: Amino Acid
TOPOLOGY: Linear
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                         Score 632; DB 12;
Pred. No. 2.1e-38;
8; Mismatches 116;
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                                                                                                                                                                                                                                                           Length 346;
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RESULT 6 US-09-978-339-2

Sequence 2, Application US Patent No. US20020103358A1 GENERAL INFORMATION:

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; LENGTH: 333
; TYPE: PRT
; ORGANISM: homo :
US-09-754-105-2
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CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: 09/329,531
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09754105 Patent No. US20010009768A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 135; Conserv
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APPLICANT: Reddy, Pranhitha
APPLICANT: REDDYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
FILE REFERENCE: 28232
FILE REFERENCE: 28232
304
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YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                              YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                      WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                           GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC
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                                                                                                                                                                                                                                                                                                                          PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
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                                                                   KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                          GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFÅGIÅSGCIIFIVIIITIVVLLL
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40.9%; Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 13;
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TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-978-339-2
WS-10-021-121-10
US-10-021-121-10
; Sequence 10, Application US/10021121
; Patent No. US20020142444A1
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Best Local Similarity
Matches 135; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GALLLLGVIGIVSGISLEPVYWNSANKRFQAEGGYVLYPQIGDRIDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seese, Kathryn A. REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2823
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/271,948
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reddy, Pranhitha ...
TITLE OF INVENTION: No. US20020103358A1el Cytokine Designated Lerk-5
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                              WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                        DYYLIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                              YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                                                                                                                        YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                        GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
                                                                                                                                                                                                                                                                                                                                                  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                                                                                                                                                              DYYTTSTSNGSLEGIDNQEGGVCQTRAMKTLMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
                                                                                                                                                                                                                    KYRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.
RENT APPLICATION DATA: 15-Oct-2001
FILING DATE: 15-Oct-2001
CLASSIFICATION: CURRONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 333 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
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Pred. No. 3.1e-38;
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RESULT 8 US-10-138-787-4

Sequence 4, Application US/10138787 Patent No. US20020172984A1 GENERAL INFORMATION: APPLICANT: Holland, Sacha

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PILING DATE: 19-Max-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-8674
TELEPHONE: 650/95-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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APPLICANT: Caras, Ingrid W
IITLE OF INVENTION: A2-1 Neurotrophic Factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WilhPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                             KYRRRHRKHSPOHTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR--
                                                                                                                    WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                     DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                           GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                         YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                             ĠRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAĞIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                             DYYIISTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                                                                                PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                           GVLMVLCRTAISKSIVLEÞIYMNSSNSKFLÞGQGLVLYÞQIGDKLDIICÞKV---DSKTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 333 amino acids
TYPE: Amino Acid
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 629.5; DB 12; Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 333;
                                                                                  -TADSVFCPH
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                                                                                                                      310
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GENERAL INFORMATION:

APPLICANT: Holland, Sacha

APPLICANT: Mbamalu, Geraldine

APPLICANT: Mbamalu, Geraldine

APPLICANT: Pawson, Tony

ITILE OF INVENTION: DIGOMERIZED RECEPTORS WHICH APFECT PATHWAYS REGULATED

ITILE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

ITILE OF INVENTION: TYROSINE KINASES

FILE REFERENCE: 11757_23USWO

CURRENT APPLICATION NUMBER: US/10/138,787

CURRENT APPLICATION NUMBER: US/09/214,631

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: PCT/CA97/00473

PRIOR APPLICATION NUMBER: PCT/CA97/00473

PRIOR APPLICATION NUMBER: 05/09/21,272

PRIOR FILING DATE: 1999-07-04

PRIOR APPLICATION NUMBER: 60/021,272

PRIOR FILING DATE: 1996-07-05

NUMBER OF SEQ ID NOS: 13
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APPLICANT: Pawson, Tony
ITILE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
ITILE OF INVENTION: BY TRANSMEWBRANE LIGANDS FOR ELK-RELATED RECEPTOR
ITILE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT AFPLICATION NUMBER: US/10/138,787
CURRENT AFPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1997-07-05
PRIOR FILING DATE: 1996-07-05
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; ORGANISM: Homo
US-10-138-787-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10138787 Patent No. US20020172984A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
33.6%; Score 622.5; DB 9;
Best Local Similarity 40.9%; Pred. No. 9.7e-38;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 135;
SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTPNKDPTRRPELEAGTN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ-SPRGGAVPRKPVSEMP-MER-DR 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNYEFYKLYLVGGAQGRRCEAPPAPNILLICDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
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                                                                                                                                                                                                                                                                                                                                                              PATHWAYS REGULATED
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APPLICANT: Holland, Sacha
APPLICANT: Holland, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: PAWSON, TONY
TITLE OF INVENTION: CLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: WG/021,272
PRIOR APPLICATION NUMBER: DCT/CA97/00473
PRIOR FILING DATE: 1996-07-05
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                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-13
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                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/10138787 Patent No. US20020172984A1 GENERAL INFORMATION:
                                                                       Query Match 20.0%;
Best Local Similarity 100.0%;
                                                                Matches
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Best Local Similarity
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252 RRRRAKPSESRHPGFGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPFFCPHY 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
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                                                                89;
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                                                            26.9%; Score 498; DB 9; 1
100.0%; Pred. No. 1.9e-29;
tive 0; Mismatches 0;
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; Pred. No. 1e-36;
50; Mismatches 116;
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                                                                                                      Length
                                                                Indels
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US-09-864-761-48262
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US-09-862-179A-17
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CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
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Best Local S
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                                                                                                                                                        PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PRIOR DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron
APPLICANT: Rank, David F
APPLICANT: Hanzel, David
APPLICANT: Chen, Wensher
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                                                                            PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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TYPE: PRT
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wenesheng
IITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROI
IITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 0/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/236,359
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 48262
LENGTH: 92
TYPEP: "SET TO SEQ ID NO 48262
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Best Local S
Matches 52
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APPLICANT: Penn, SI
APPLICANT: Rank, I
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR TILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Pred. No. 4.1e-14;
5; Mismatches 24
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITILE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PALOS

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PET/US/00/05989

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270
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                                   PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 639
LENGTH: 106
TYPE: PRT
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US-09-925-297-639
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Best Local
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ORGANISM: Homo sapiens
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PRIOR
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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Pred. No. 3e-
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Sequence 15, Application US/09862179A

Patent NO. US20020147306A1

PATENT INFORMATION:
APPLICANT: Lin, Danny
APPLICANT: Lin, Danny
ITITLE OF INVENTION: PEPTIDES THAT MODULATE THE INT
ITITLE OF INVENTION: AND PDD DOWAINS
FILE REFERENCE: MTG1-P01-009

CURRENT FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.1

SEQ ID NO 15
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 199-03-12
PRIOR FILING DATE: 199-07-04
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-11
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US-10-138-787-11
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US-09-862-179A-15
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Best Local Similarity
Matches 44; Conserv
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Best Local Similarity
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APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED REC
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
TYPE: PRT
ORGANISM: Homo sapiens
                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 RRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEPGELGIALRGGGAADPPF 307
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Pred. No. 3.6e-08;
9; Mismatches 24
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US-09-862-179A-16
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Best Local Similarity 47.3
Matches 44; Conservative
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Best Local Similarity
Matches 38; Conserv
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SEQ ID NO 12
LENGTH: 82
TYPE: PRT
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Query Match
                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pawson, Tony
TITLE OF INVENTION: DLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
TILE REFERENCE: 11757 23USWO
CURRENT FILLING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR RILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 605/021,272
PRIOR APPLICATION NUMBER: 605/021,272
                                                                                                                                                               APPLICANT: Lin, Danny
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
TITLE OF INVENTION: AND PDZ DOMAINS
TILE REPERENCE: MTSI-P01-009
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 44
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APPLICANT: Pawson, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                          LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 AEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 RRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEPGELGIALRGGGAADPPF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 SEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKRHRKHTQQ------RAAALSLSTLASPKGGSGTAGTEPSDIIIPLR---TTENNY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10138787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geraldine
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  10.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 201; DB 10;
Pred. No. 3.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 200.5; DB 9;
Pred. No. 3.9e-08;
4; Mismatches 8;
    Score 200.5;
    B
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    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 82;
  Length 82;
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TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: S
US-09-904-954-2
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US-09-904-954-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 71.7 Matches 38; Conservative
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
127
                                      118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/904,954
FILING DATE: 12-Jul-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-193
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-193
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ^{3}_{3}
                                                                            83
                                                                                                             65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                                                                                                          7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRPQAEGGYVLYPQIGDRLDLLCP--R 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CERRETTI, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BECKMANN, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
                               QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
                                                                         SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126
                                                                                                                                                                                                                                        65
'
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: SEATTLE STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: IMMUNEX COF
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                        GALG-----NRHAVYWNSSNOHLRRE-GYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMUNEX CORPORATION
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                                                                                                                                                                                                                                                         28.4%;
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                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                        24;
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                                                                                                                                                                                                                                      Score 179; DB 10;
Pred. No. 4.4e-06;
4; Mismatches 80
                                                                                                                                                                                                                                                                                                                                         ID NO:
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                                                                                                                                                                                                                                                                            Length 238;
                                                                                                                                                                                                                                          Indels
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TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-921-984-2
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US-09-921-984-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 227-5;
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223
                                                                                                                   145 REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 RKPVSEMP-----PGKENLP 204
                                                                                                                                                              94 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151
                                                                                                                                                                                                  88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                                                                                                                                                                                                                                           35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
                                                                                                                                                                                                                                                                               33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Flanagan, John G.
APPLICANT: Flanagan, John G.
Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36.709
REFERENCE/DOCKET NUMBER: HMI-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/921,984
FILING DATE: 31-Uul-2001
CLASSEFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(txt)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
EAPEPIFTSNSSCSGLGG 192
                                    GDP----TSNATSRGAEG 218
                                                                               ----PNLVDRPCLR--LKVYVR-
                                                                                                                                                                                                                                                                                                                            .
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/308,814 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TY: Boston
                                                                                                                                                                                                                                                                                                                            Conservative
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(617) 227-5941
                                                                                                                                                                                                                                                                                                                                         9.5%;
                                                                                                                                                                                                                                                                                                                        ; Score 176; DB 9;
; Pred. No. 6.2e-06;
19; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                            Length 209;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                     52; Gaps
                                                                               PINETLY 174
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7;

RESULT

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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 510
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-7
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                                                                                              ; ORGANISM: Homo sapiens 
US-09-925-297-510
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US-09-925-297-510
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Patent NO. US20020172984A1

GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Moamalu, Geraldine
APPLICANT: Pawson, Tony
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757. 33USWO
CURRENT APPLICATION NUMBER: US/10/136,787
CURRENT PILING DATE: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 510, Application US/09925297 Patent No. US20020081659A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 174.5; Best Local Similarity 27.4%; Pred. No. 9e-
                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 -----PGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 EFHAGHEYYYISTPTHNLH------WKCLR--MKVFVCCASTSHSG---EKPVPTLPQF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 EFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 YVLYMVSRNGYRTCNASOGFKRWECNRPHAPH-----SPIKFSEKFORYSAFSLGY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYNSSGAGPGPGGGAE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 GVLGLVSGLSLEÞVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR----ARPPGPHSSPN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEFYKLYLVG-----GAQGRR----CEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
  Conservative
                      28.3%;
    30;
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  Score 172.5; DB:
Pred. No. 1.2e-05
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 9e-06;
74;
                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
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    Indels
                                            Length 218;
    19;
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    Gaps
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; Sequence 4, Application US/09904954
; Patent No. US20020010325A1
; GENERAL INFORMATION:
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                                                                                                                             Query Match
Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                  TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
    83
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                                                                                                                                                  Local Similarity
                                                                                 24 LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/240,124
FILING DATE: <UNKNOWN:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                             NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
ATTREFT: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BECKMANN, M. P.
CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
    LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTPFTLGKEFKEGHSYYYISKPIHQHEDR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARPPGPHSSPN--YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQE 119
                                              IRGGSSIRHVVYWNSSNPRI-IRGDAVVELGINDYIDIVCPHYEGPGPPEGP--ETFALY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGQARAMEFLWAPLLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGVRVGALLLLGVLGLVSGLSL---EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR
                                                                                                                             66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-Jul-2001
CLASSIFICATION: JUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                               Conservative
                                                                                                                                              9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR HEK
                                                                                                                             18;
                                                                                                                          Score 169.5; DB 10;
Pred. No. 1.7e-05;
8; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -CLRLKVTVSGKITHSPQAHDNPQE 176
                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version
                                                                                                                               Indels
                                                                                                                                                                    Length 201;
                                                                                                                             55;
                                                                                                                             Gaps
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APPLICANT: Modmail, Sacha
APPLICANT: Modmail, Geraldine
APPLICANT: Modmail, Geraldine
APPLICANT: Modmail, Geraldine
APPLICANT: Modmail, Geraldine
TITLE OF INVENTION: DI-GOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT PILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1997-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-138-787-8
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US-10-138-787-6
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                                                                                                                                                        Sequence 6, Application US/10138787
Patent No. US20020172984A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10138787 Patent No. US20020172984A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                 APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                      188
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les 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LLLGVL-----GLVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPP 68
REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVFRKPVSEMPME 187
                                                                                                                                                                                                                                                                                                                          RKSESAHPV-----
                                                                                                                                                                                                                                                                                                                                                                    RDRGAAHSLEPGKENLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPPEGP--ETFALYMYDWPGYESCQÁEGPRGYKRWVCSLPFGHVQPSEKIÓRFTPFSLGF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPHSSPNYEFYKLYLVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLITVLWAAFLGSPLRGGSSLRHVVYWNSSNPR-SLRGDAVVELGLNDYLDIVCPHYEGP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 169; DB 9; ilarity 29.8%; Pred. No. 1.9e-05; Conservative 19; Mismatches 84
                                                                                                                                                                                                                                                                                                                          -GSPGESGTSGWRGGDTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RLQVSVCCKERKSESAHPV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 201;
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                                                                                                                                                                                                                                                                                                                            LCLLLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
FRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1996-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 209
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                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/330128

FILING DATE: 27-0CT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486449

FILING DATE: 06-0TU-1995

ATTORNEY/AGENT INFORMATION:

RAGISTRATION NUMBER: 36,700

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P0920P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -08-578-684-4
                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDITM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 GHASCDHRORGEKRWECNRPAAPGGPLKFSEKFOLFTPESLGFEFPPGHEYYYISAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 VYWNRSNPRFOVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 YYWNSANKRFOAE----GGYVLYPOIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
    IOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94080
                        Amino Acid
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Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                        02-Jan-1996
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.1%; Score 168.5; DB 9;
35.9%; Pred. No. 2.2e-05;
ative 14; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Sequence 10, Application US/10138787

Patent No. US20020172984A1

GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: DIGOMERIZED RECEPTORS WHICH
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: 00/021,272
PRIOR APPLICATION NUMBER: 00/021,272
PRIOR APPLICATION NUMBER: 00/021,272
PRIOR PILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
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Best Local S
Matches 65
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LENGTH: 205
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124 HSYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHVNPQE 163
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                                     133 HDYYIJATSDGTREGLESLQGGVÇLTRGMKVLLRVGQSPRGGAVPRK 179
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                                                                                    64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 123
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Local Similarity 27.5%;
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                                                                                                                               YEFYKLYLVGGAQGRRCBAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
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                                                                                                                                                                           LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVOLNDYVDIICPHYE---DHSVADAA 63
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; Pred. No. 2.8e-05; 
29; Mismatches 81;
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US-10-001-054-48
; Sequence 48, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: CELL GROWTH
FILE REPERENCE: 9309481PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
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OR FILING DATE: 1998-12-15
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OR APPLICATION NUMBER: 60/115554
OR FILING DATE: 1998-12-22
OR APPLICATION NUMBER: 60/115558
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OR APPLICATION NUMBER: 60/083545

OR FILING DATE: 1998-04-29

OR APPLICATION NUMBER: 60/085149

OR FILING DATE: 1998-05-12

OR APPLICATION NUMBER: 60/087607

OR FILING DATE: 1998-06-02
DR FILING DATE: 1999-06-22

DR APPLICATION NUMBER: 60/141037

DR FILING DATE: 1999-06-23

DR APPLICATION NUMBER: 60/144758

OR FILING DATE: 1999-07-20

DR APPLICATION NUMBER: 60/142506

OR APPLICATION NUMBER: 60/170262

OR APPLICATION NUMBER: 60/170262

OR FILING DATE: 1999-12-09
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APPLICATION NUMBER: 60/1
FILING DATE: 1999-04-07
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APPLICATION NUMBER: 60/108849
FILING DATE: 1998-11-18
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Gurney, Austin
Hebert, Carolyn
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Kabakoff, Rhona
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PRIOR FILING DATE: 2000-03-03
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IOR APPLICATION NUMBER: 09/941992
IOR FILING DATE: 2001-08-04
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IOR FILING DATE: 1990-09-10
IOR APPLICATION NUMBER: PCT/US98/18824
IOR FILING DATE: 1998-09-10
IOR APPLICATION NUMBER: PCT/US99/00106
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IOR APPLICATION NUMBER: PCT/US99/05028
IOR FILING DATE: 1999-01-05
IOR FILING DATE: 1999-01-05
IOR FILING DATE: 1999-04-20
IOR FILING DATE: 1999-06-02
IOR APPLICATION NUMBER: PCT/US99/1225
IOR APPLICATION NUMBER: PCT/US99/20111
IOR APPLICATION NUMBER: PCT/US99/20513
IOR APPLICATION NUMBER: PCT/US99/20513
IOR APPLICATION NUMBER: PCT/US99/20513
IOR APPLICATION NUMBER: PCT/US99/28313
IOR APPLICATION NUMBER: PCT/US99/28551
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OR FILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/US99/28634
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OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: 1999-12-16
OR APPLICATION NUMBER: PCT/US99/3099
OR FILING DATE: 1999-12-20
OR APPLICATION NUMBER: PCT/US00/00376
OR APPLICATION NUMBER: PCT/US00/00376
OR FILING DATE: 2000-01-06
OR APPLICATION NUMBER: PCT/US00/03565
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R APPLICATION NUMBER: 09/924419
DR FILING DATE: 2001-08-06
DR APPLICATION NUMBER: 09/927796
DR FILING DATE: 2001-08-06
PR APPLICATION NUMBER: 09/929404
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APPLICATION NUMBER: 09/866034
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; LENGTH: 204
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US-10-001-054-48
                                                                 RESULT 29
US-10-028-072-288
; Sequence 288, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
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Best Local Similarity 27.7
Matches 46; Conservative
  APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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APPLICATION NUMBER: PCT/US01/27099
FILING DATE: 2001-08-29
R OF SEQ ID NOS: 91
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APPLICATION NUMBER: PCT/US01/06666
APPLICATION NUMBER: PCT/US01/06666
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APPLICATION NUMBER: PCT/US00/30873
FILING DATE: 2000-11-10
APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US00/14941
FILING DATE: 2000-05-30
APPLICATION NUMBER: PCT/US00/15264
FILING DATE: 2000-06-02
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APPLICATION NUMBER: PCT/US00/14042
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FILING DATE: 2000-03-30
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APPLICATION NUMBER: PCT/US01/21066
FILING DATE: 2001-06-29
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FILING DATE: 2001-06-20
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APPLICATION NUMBER: PCT/US00/23522
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APPLICATION NUMBER: PCT/US00/06884
FILING DATE: 2000-03-15
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APPLICATION NUMBER: PCT/US01/17092
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APPLICATION NUMBER: PCT/US00/05841
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                                                                                                                                                                                                                                                                                   DYYLLATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
                                                                                                                                                                                                                                                                                                                                EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
                                                                                                                                                                                                                                                                                                                                                                           EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
DeForge, Laura
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27.7%; Pred. No. 4.1e-05;
vative 31; Mismatches 74; Indels
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PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059713
PRIOR FILING DATE: 1997-09-17
PRIOR PPLICATION NUMBER: 60/059113
PRIOR PPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/05917
PRIOR APPLICATION NUMBER: 60/05917
PRIOR APPLICATION NUMBER: 60/05917
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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OR APPLICATION NUMBER: 60/063329
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063550
OR APPLICATION NUMBER: 60/063561
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OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/05988
OR APPLICATION NUMBER: 60/059836
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/062280
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062287
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062814
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OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059122
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059184
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059263
OR FILING DATE: 1997-09-18
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FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063735
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063738 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063755
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APPLICATION NUMBER: 60/063704
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APPLICATION NUMBER: 60/063561
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Watanabe, Colin
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Stewart, Timothy A.
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Filvaroff, Ellen
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/64248
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/064809
OR FILING DATE: 1997-11-07
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17
OR APPLICATION NUMBER: 60/066364

FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/069212
FILING DATE: 1997-12-11

APPLICATION NUMBER: 60/066453 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/066511

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APPLICATION NUMBER: 60/069278 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069334

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OR FILING DATE: 1998-05-22
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OR APPLICATION NUMBER: 60/088726
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OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091360
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OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085579
OR APPLICATION NUMBER: 60/085697
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                                       DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
                                                                                          EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
                                                                                                                                       EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH:133
                                                                                                                                                                                               LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVOLNDYVDIICPHYE---DHSADAAM
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                                                                                                                                                                                                                                                                                                                      Similarity
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ilarity 27.7%;
Conservative 3
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CIRLKVTVSGKITHSPQAHDNPQE 162
                                                                                                                                                                                                                                                                                              Score 164.5; DB 9;
Pred. No. 4.1e-05;
1; Mismatches 74;
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OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069694
OR FILING DATE: 1997-12-16
OR APPLICATION NUMBER: 60/072320
OR FILING DATE: 1998-01-23
OR APPLICATION NUMBER: 60/073612
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074096
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074092
OR APPLICATION NUMBER: 60/07791
OR FILING DATE: 1998-03-09
OR APPLICATION NUMBER: 60/07791
OR FILING DATE: 1998-03-12
OR FILING DATE: 1998-03-12
OR FILING DATE: 1998-03-10
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294

PRIOR

OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-02-27
OR APPLICATION NUMBER: 60/079728
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/080165
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/081203

OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081229
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081695
OR FILING DATE: 1998-04-14
OR APPLICATION NUMBER: 60/081817

FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082999
FILING DATE: 1998-04-24
APPLICATION NUMBER: 60/083322

FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081818

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FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083545

FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084627

FILING DATE:

1998-05-07

RESULT 30
US-10-121-049-288
; Sequence 288, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Beresini, Maureen
; APPLICANT: Beresini, Maureen

OR APPLICATION NUMBER: 60/084637
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085149
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13

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; ORGANISM: Homo Sapien
US-10-121-049-288
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Best Local Similarity
Matches 46; Conserv
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LENGTH: 204
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
                                                      APPLICANT: Zhang, Zemin
TITLE OP INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OP INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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                     CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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NUMBER OF SEQ ID NOS: 550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
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                                                                                                                         Tumas, Daniel
Watanabe, Colin K
Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
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See File Wrapper or Palm
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; ORGANISM: Homo Sapien
US-10-140-470-288
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-288
                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local Similarity 27.7'
Matches 46; Conservative
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SEQ ID NO 288
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 2002-05-06
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134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
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                                                                                                                                                                           18 LIGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS-PNY 76
                                                           64 EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
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                                                                                             EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                       LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSADAAM 63
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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27.7%; Pred. No. 4.1e-05;
ative 31; Mismatches 74
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;; Pred. No. 4.1e-05;
31; Mismatches 74; Indels
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-175-746-288
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publication No. US200:
GENERAL INFORMATION:
APPLICANT: Baker, Kev
APPLICANT: Beresini
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Matches
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APPLICANT: Baker, Kevin P.
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/175,746

CURRENT FILING DATE: 2002-06-19
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Local Similarity 27.7%;
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Godowski, Paul J.
Gurney, Austin L.
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                                   Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
                                                                                             Gao, Wei-Qiang
Gerritsen, Mary E.
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Filvaroff, Ellen
              Sherwood, Steven
                                                                                                                                                                           DeForge,Laura
                                                                                                                                                                                             Beresini,Maureen
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Filvaroff, Ellen
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o. US20030027270A1
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Camin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: p330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION TEMPORED FOR THE Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
TYPE: PRT
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                                                                               US-10-176-921-288
                                                                                                                                 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 288 LENGTH: 204
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Publication No.
    Matches
                  Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C288 CURRENT APPLICATION NUMBER: US/10/176,921 CURRENT FILING DATE: 2002-06-20
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                                                                                             ORGANISM: Homo Sapien
                                                                                                                  TYPE: PRT
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46;
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Filvaroff, Ellen
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  Conservative
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                  8.9%; Score 164.5;
27.7%; Pred. No. 4.1
    Mismatches
                    4.1e-05
                                     DB 9;
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CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1997-07-05
PRIOR FILING DATE: 1996-07-05
VUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 228
                                                                                                                                                                                                   RESULT 37
US-09-925-301-1225
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US-10-138-787-9
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Patent No. US20020172984A1
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYROSINE XINASES
FILE REFERENCE: 11757.23USWO
                                                                                                                                  Sequence 1225, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
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            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
  PRIOR APPLICATION NUMBER: PCT/US00/05882
                                                                                                                                                                                                                                                                                             187 PADDTV---HESAEPSRG-ENAAQTPRIPSRL-----LAILLFLLA 223
                                                                                                                                                                                                                                                                                                                                             198
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8.7%; Score 160.5; DB 9;
Local Similarity 28.3%; Pred. No. 8.9e-05;
hes 64; Conservative 29; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
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                                                                                         and Antibodies
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                                                                                                          US-10-001-887-108
; Sequence 108, Application US/10001887
; Patent NO. US20020155464A1
; GENERAL INFORMATION:
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US-09-862-179A-2
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TITLE OF INVENTION: APPTIDES THAT MODULATE THE INTERACTION OF
TITLE OF INVENTION: AND PDZ DOMAINS
FILE REFERENCE: WISI-P01-009
CURRENT PILLING DATE: 2001-05-21
NUMBER OF SEC ID MOS: 44
SOFTWARE: Patentin version 3.1
SEC ID MO 2
LENGTH: 28
TYPE: PRT
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SEQ ID NO 1225
LENGTH: 27
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Best Local Similarity 100.0%;
Matches 27; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                              APPLICANT: Salceda, Susana APPLICANT: Macina, Roberto
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
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OTHER INFORMATION: Xaa=Ala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa=Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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Sun,
                     Recipon, Herve
Cafferkey, Robert
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  Yongming
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Pred. No. 0.00022
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US-09-823-240-10
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                                                                                 Query Match
Best Local S
Matches 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 138; DB 9
Best Local Similarity 27.9%; Pred. No. 0.011;
Matches 68; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 108
LENGTH: 638
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT: Jurgen Wehland
APPLICANT: Joseph Lourelo
ITITLE OF INVENTION: Methods and Products for Regulating Cell
ITITLE OF INVENTION: Mothlity
FILE REFERENCE: MO556/7064 (HGL)
CURRENT APPLICATION NUMBER: US/09/823,240
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/194,564
PRIOR APPLICATION NUMBER: 60/194,564
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes
FILE REFERENCE: DEX-0269
CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR FILING DATE: 60/249,998
PRIOR FILING DATE: 2000-11-20
PRIOR PPLICATION NUMBER: 60/249,998
PRIOR FILING DATE: 2000-11-20
PRIOR PPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Frank B. Gertler APPLICANT: James E.Bear
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                          ORGANISM: Homo sapien
                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 RGMKVLLRVGQ-----SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATS
  16
                                        35 WNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEA 94
                                                                                 Local Similarity 22.8
les 67; Conservative
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    YDDGNKRWLPAG---TGPQAFSRVQI---
                                                                                                                                                                                                                                   380
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                                                                                 7.1%; Score 130.5; DB
22.8%; Pred. No. 0.022;
ative 34; Mismatches 1
                                                                               34;
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    -YHNPTANSFRVV---
                                                                                                                          DB 10;
                                                                                 102;
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                                                                                    Indels
                                                                                                                        Length 380;
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                                                                                    91;
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    GRKMQ- 55
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: BC/124,270
PRIOR APPLICATION NUMBER: BC/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 979
LENGTH: 674
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-979
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                                                                                                                            RESULT 42
US-09-854-133-187
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US-09-925-299-979
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Sequence 187, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
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Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 SRGER-GLPGVAGAV----GEPGPLGIAGPPGARGPPGAVGSPGVNGAPGEAGRDGNPGN 240
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                                                                                                                                                                                                              GGYDFGYDGDFYRADQPRSAPSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDGTREGLESLQGGVCLTRGMKVLLRVGQSP--RG--GAVPRKPVSEMPME--RDRGAAH 194
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                                                                                                                                                                                                                                                         --- DYGHPVYIVQDGPPQSPPNI 336
                                                                                                                                                                                                                                                                                                                                                                                    GA-----VGPRGPSGPQGIRGDKGEPGEKGPRGLPGLKGHNGLQGLPGIAGHHGDQGAPG 353
                                                                                                                                                                                                                                                                                                                                                                                                                             GGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSLGL------GGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAPNILLICORPOLDIRFTIKFQEYSPN-----LWGHEFRSHHDYYIIATSDGTR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%; Score 130.5; DB 10; ilarity 27.4%; Pred. No. 0.042; Conservative 20; Mismatches 92;
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                                                                                                                                                                                                                                                                                                                                              -----REAEPGELGIA-LRG------GGAADPPFCPHYEKVSG 316
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US-09-738-973-187
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                                                                                    US-09-738-973-187
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 187
LENGTH: 595
TURNET: 595
                                                                                                                                      FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 187
LENGTH: 595
Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 187, Application US/09738973 Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 69;
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                     APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                   TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMGRQHEAAATAATAATATGGTAEEAGASAPES----QAGGGPRGRA--RGPRQQGRRR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFRSHIDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSE---- 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
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Benson, Darin R.
Elliot, Mark
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Secrist, Heather
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0%; Score 129; DB 9; Length 595; ilarity 27.4%; Pred. No. 0.047; Conservative 18; Mismatches 89; Indels
    Conservative
                                                                                                     sapier
                                                                                                                                                                                      for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raodoh
  7.0%; Score 129; DB 10; Length 595;
27.4%; Pred. No. 0.047;
tive 18; Mismatches 89; Indels 7
                                                                                                                                                                                                                                                                                          LUNG CANCER
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    76;
    Gaps
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56, Application US/09919497

Patent No. US20020106662A1

GENERAL INFORMATION:

APPLICANT: Mutter, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225

FILE REFERENCE: B0801/7225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1806
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: UNSURE
LOCATION: (758) . (758)
OTHER INFORMATION: Xaa =
                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE
LOCATION: (809)..(809)
722
                                                                                                                                                                                                                                      561 QGPRGVQGPPGPTGK-PGKRGRPGADGGRGMPGEPGAKGDRGFDGLPGLPGDKGHRGERG
                                                                                                                                                                                                                                                                          169 QSPRGGAVPRKPVSEMPMER-----DRGAAHSLEPGKE-----NLPGD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 HGTQRRRGPPQAREEG----PRDATTILGLGTPSGEQRADQSQALPALAGAAAAHAHAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 MPMERDRGAAHSLEPGKENLPGDPTS---NATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 GGAESPRGWEAGP--
                                                                                                                                                                                                                                                                                                                 Local Similarity
tes 64; Conserv
  LAGLPGADGPPGHPGKEGQSGEKG----ALGPPGPQGP 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMGRQHEAAATAATAATATGGTAEEAGASAPES-----QAGGGPRGRA--RGPRQQGRRR 254
                                      ----GAADPPFCPHYEKVSGDYGHPVYIVQDGP--PQSP 333
                                                                            PGMAGVDGPPGPKGNMGPQGEPGPPGQQGNPGPQGLPGPQGPIGP----PGEKGPQGKPG
                                                                                                                                                        PQGPPGPPGDDGMRGEDGEIGPRGLPGEAGPRG-----LLGPRGTPGA-----
                                                                                                                                                                                              -----PTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGRGGGAAGP 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSE----
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                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                    7.0%;
29.1%;
                                                                                                                  -- SRHPG-PGSFGRGGSLGL-GGGGGMGPREAEPGELGIALRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             any amino
                                                                                                                                                                                                                                                                                                                 Score 129; DB
Pred. No. 0.16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----REWGPSPSGHGDGPRRRPRKRRGRKG 201
                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 1806;
                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                       13;
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RESULT 45 US-09-925-302-689 ; Sequence 689, A

Application US/09925302

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APPLICATION ROSEN et al.

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

SOFTWARE: Patentin Ver. 2.0
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US-09-978-295A-614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 46; Conserv
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                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (183)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                       APPLICANT
                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 GVMGP--PGAQGSKGDFGRP-----GPP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 PGKENLPGDPTSNATS-----RGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AADPPFCPHYEKVSGDYGHPVYIVQDGPP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRRAKPSESRHPGP----GSFGRGGSLGLGGGGGGGGREAEPGELGI-----ALRGGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO. US20020044941A1
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KQGATGTPGPQGEKGSKGDGGLIGPKGETG---TKGEKGDLGLPGSKGDRGMKGDA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403
INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashkenazi, AviBaker Kevin P.Botstein, DavidDesnoyers, Luc
                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                        Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
              Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                          Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                   Fong,
                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                        Paoni, Nicholas F.
                                                                                                                                                                                Napier,
                                                                                                                                                                                                                         Kljavin,
                                                                                                                                                                                                                                          Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                         Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                            win, Ivar J.
Sophia S.
Ler, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                    Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                     Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dan
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30.9%;
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Pred. No. 0.046;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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PRIOR APPLICATION NUMBER: 60/07
PRIOR FILING DATE: 1998-03-12
PRIOR PRIOR PRICICATION NUMBER: 60/07
PRIOR PRILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/07)
PRIOR APPLICATION NUMBER: 60/07)
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/07
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07
PRIOR REILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07
PRIOR APPLICATION NUMBER: 60/07
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PRIOR APPLICATION NUMBER: 60/06
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06
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PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 1998-03-
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                                                                                               OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079786
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079920
OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/079923
OR APPLICATION NUMBER: 60/079923
OR APPLICATION NUMBER: 60/080105
                                                                                                                                                                                                 DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/0
DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/0
DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/0
DR FILING DATE: 1998-04-01
DR FILING DATE: 1998-04-01
DR FILING DATE: 1998-04-01
DR APPLICATION NUMBER: 60/0
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R APPLICATION NUMBER: 60,

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60,

R APPLICATION NUMBER: 60,
                                                                                FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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                       FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-03-APPLICATION NUMBER: 6
                                                                                                                                                               FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C11

FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817

APPLICATION NUMBER: 60/081955

FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081952

APPLICATION NUMBER: 60/081819 FILING DATE: 1998-04-15

FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081838

FILING DATE: 1998-04-1

FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09

FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203

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RESULT 47
US-09-978-697-614
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Best Local S
Matches 46
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Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-15
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085682
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
OR APPLICATION NUMBER: 60/085689
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/08579
OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085697
OR APPLICATION NUMBER: 60/085704
OR APPLICATION NUMBER: 60/085704
OR APPLICATION NUMBER: 60/085697
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46; Conserv
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Goddard, Audrey
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                           Gurney, Austin L. Hillan, Kenneth J Kljavin, Ivar J. Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi, Avi
Baker Kevin P.
Botstein, David
Desnoyers, Luc
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                                                                                                       Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
                                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, J. Christopher
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Ferrara, Napoleon
Filvaroff, Ellen
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ilarity 30.9%;
Conservative
                    Daniel
ms, P. Mickey
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OR AFFLICATION NUMBER: 60/083558
OR FILING DATE: 1998-04-29
OR AFFLICATION NUMBER: 60/083559
OR AFFLICATION NUMBER: 60/08359

FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083554 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083499

FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496

FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392

APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27

APPLICATION NUMBER: 60/083322

APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-23

FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804

FILING DATE

: 1998-04-22

APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21

FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30

R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/01
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/01
R APPLICATION NUMBER: 50-07

NUMBER: 60/084640

60/084598

APPLICATION NUMBER: 60/084441 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07

APPLICATION NUMBER: 60/084639

FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/084414 APPLICATION NUMBER: 60/084366

FILING DATE

1998-05-06

R APPLICATION N FILING DATE: R APPLICATION N FILING DATE:

NUMBER: 60/084600 : 1998-05-07

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PRIOR FILING DATE: 1998-05-05 PRIOR APPLICATION NUMBER: 60/084414 PRIOR APPLICATION NUMBER: 60/084411 PRIOR APPLICATION NUMBER: 60/084441 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/084637 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084639 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084598 PRIOR APPLICATION NUMBER: 60/084500 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-04-28 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083495 PRIOR APPLICATION NUMBER: 60/083495 PRIOR FILING DATE: 1998-04-29 PRIOR PPLICATION NUMBER: 60/083496 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083545 PRIOR APPLICATION NUMBER: 60/083545 PRIOR APPLICATION NUMBER: 60/083545 PRIOR FILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083554 PRIOR APPLICATION NUMBER: 60/083559 PRIOR APPLICATION NUMBER: 60/083559 PRIOR APPLICATION NUMBER: 60/083559 PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083500 PRIOR FILING DATE: 1998-04-39 PRIOR APPLICATION NUMBER: 60/083500 PRIOR APPLICATION NUMBER: 60/083500 PRIOR APPLICATION NUMBER: 60/08354	

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RESULT 48
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Best Local S
Matches 46
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Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botestein, David
APPLICANT: Botestein, David
APPLICANT: Desnoyers, Luc
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OR APPLICATION NUMBER: 60/084643
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/08533
OR APPLICATION NUMBER: 60/08533
OR APPLICATION NUMBER: 60/08532
OR APPLICATION NUMBER: 60/085323
OR APPLICATION NUMBER: 60/08582
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085582
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
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OR APPLICATION NUMBER: 60/085579
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OR APPLICATION NUMBER: 60/085704
OR APPLICATION NUMBER: 60/085697
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
                             Stewart,
Tumas, I
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                                             Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                            Paoni,
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  Williams,
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llarity 30.9%;
Conservative
                                                                                                                                                         James;
                                                                                                                                                                                                      Sophia S.
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                                                                                                                         Nicholas F.
                                                                                                                                                                            , Mary A.
                               Daniel
     P. Mickey
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Pred. No. 0.061;
9; Mismatches
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PRIOR PILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/063449
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07791
PRIOR APPLICATION NUMBER: 60/078904
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/079636
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079663
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
OR APPLICATION NUMBER: 60/080333
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080334
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/081070
OR APPLICATION NUMBER: 60/081049
OR APPLICATION NUMBER: 60/081049
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R APPLICATION N
R FILING DATE:
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FILING DATE: 1998-03-31
                                                                                                                                                                                                      NUMBER: 60/080328
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OR APPLICATION NUMBER: 60/08359
OR FILING DATE: 1998-04-29
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083500
OR APPLICATION NUMBER: 60/083742
OR APPLICATION NUMBER: 60/084366
OR RILING DATE: 1998-04-30
OR APPLICATION NUMBER: 60/084366
OR APPLICATION NUMBER: 60/084366
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OR APPLICATION NUMBER: 60/083392

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OR APPLICATION NUMBER: 60/083495

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OR APPLICATION NUMBER: 60/083496
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DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082700
DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082797
DR FILING DATE: 1998-04-22
DR FILING DATE: 1998-04-22
DR FILING DATE: 1998-04-26
DATE: 1998-04-27
                                                                                                                                                                                                                          FILING DATE: 1998-05-06
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APPLICATION 1998-05-06
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APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/084637
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084639
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/081817
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                                                                       APPLICATION NUMBER: 60/084598
                                                                                            APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07
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NUMBER: 60/084600
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RESULT 49 US-09-999-832A-614

Sequence 614, I Publication No. GENERAL

Application US/09999832A 5. US20020192706A1

APPLICANT: Ashkenazi, APPLICANT: Baker Kevi

Botstein, David Desnoyers, Luc shkenazi, Avi Baker Kevin P

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INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Pan, James; Paoni, Nicholas F. Roy, Margaret Ann Shelton, David L. Stewart, Timothy A.

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.

APPLICANT: APPLICANT: APPLICANT:

Filvaroff,

Napoleon f, Ellen

Fong,

Sherman

APPLICANT: APPLICANT:

Gerber, Hanspeter Gerritsen, Mary E.

Wei-Qiang

Goddard

Audrey

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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
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PRIOR APPLICATION NUMBER: 60/085323
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PRIOR APPLICATION NUMBER: 60/085582
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OR APPLICATION NUMBER: 60/085580
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OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
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OR APPLICATION NUMBER: 60/085697
268 GVMGP--PGAQGSKGDFGRP-----GPP 288
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OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
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OR APPLICATION NUMBER: 60/085579
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                                                                                                              RRRAKPSESRHPGP----GSFGRGGSLGLGGGGGMGPREAEPGELGI-----ALRGGG 301
                                    WYDE ŁECHKEKASCHŻACH KALACH W 330
                                                                             ----KQGATGTPGPQGEKGSKGDGGLIGPKGETG---TKGEKGDLGLPGSKGDRGMKGDA 267
                                                                                                                                                                                            PGKENLPGDPTSNATS-----RGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWR 252
                                                                                                                                                       PGAPGPPGPPAEKGAKGAMGRDGATGPSGPQGPPGVKGEAG---
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Similarity 30.9%;
46; Conservative
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Pred. No. 0.061;
9; Mismatches 53;
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084643

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Matches 46
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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OR APPLICATION NUMBER: 60/085579
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OR APPLICATION NUMBER: 60/085580
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PR APPLICATION NUMBER: 60/08582
OR FILING DATE: 1998-05-15
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OR APPLICATION NUMBER: 60/085339

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OR APPLICATION NUMBER: 60/085323
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Similarity 30.9%;
Roy, Marg
Shelton,
Stewart,
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                                                                                             Kuo,
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Godowski, Paul J.
Grimaldi, J. Christopher
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                                            Paoni,
                                                                                                                                        Gurney,
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Gerritsen, Mary E.
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Filvaroff, Ellen
                                                                                                            Kljavin,
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                                                                Pan,
                                                                          Napier, Mary A.
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illan, Kenneth J
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, Margaret Ann
lton, David L.
vart, Timothy A.
                                                                James;
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                                                                                           Sophia S.
                                                                                                                                                                                                                                                    Sherman
                                              Nicholas F
                                                                                                          Ivar J.
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078939
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/079786
PRIOR APPLICATION NUMBER: 60/079920
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR PRILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR APPLICATION NUMBER: 60/077791
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080327
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080328
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080333
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Williams, P. Mickey
Wood, William I.
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OR APPLICATION NUMBER: 60/084366
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OR FILING DATE: 1998-05-06
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OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082704
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OR APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/08336
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-08
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OR FILING DATE: 1998-5-07
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OR APPLICATION NUMBER: 60/08582
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OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085699
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085580
OR APPLICATION NUMBER: 60/085590
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GVMGP--PGAQGSKGDFGRP-----
                                               AADPFFCPHYEKVSGDYGHPVYIVQDGPP
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Search completed: February 11, 2003, Job time : 20.5409 secs 12:13:17

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Title:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Q8tbh7 homo sapien
Q90231 brachydanio
Q9pt69 senopus lae
Q9puj4 gallus gall
Q90233 brachydanio
Q90232 brachydanio
Q90232 brachydanio
Q90469 xenopus lae
Q9u372 caenorhabdi
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Q9431 brachydanio
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  Q9PT69;
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Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.,
"Morphogenesis of prechordal plate and notochord requires intact
"Morphophrin b signaling.";
Eph/ephrin b signaling.";
Dev. Biol. 234:470-482(2001).
EMBL; AF37527; AAK64277.1; -.
InterPro; IPR001799; Ephrin.
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ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; UNKNOWN 1.
SEQUENCE 331 AA; 35638 MW; 6ASEACD509A09818
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Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
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Teleostei; Ostariophysi;
                           PRT;
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Best Local Sim
Matches 192;
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OPPUJ4,
OPPUJ4,
O1-MAY-2000 (TrEMBLrel. 1
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O1-JUN-2001 (TrEMBLrel. 1
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SIGNAL
SEQUENCE
                                                                                            Archosauria; Aves; Gallus.
                                                                                                                                                      Ephrin-B2 precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
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Helbling P.M., Saulnier D.M.E., Robinson V., Christ
Wilkinson D.G., Brandli A.W.;
"Comparative analysis of embryonic gene expression
"teraction sites for xenopus EphB4 receptors with
Dev. Dyn. 216:361-373(1999).
EMBL; AJ236866; CAB65511.1; -.
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Kenopus laevis (African clawed frog).

Eukaryota, Metazoa, Chordata, Craniata, Venamphibia, Batrachia, Anura, Mesobatrachia,

Xenopodinae, Xenopus.
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                      NCBI_TaxID=9031;
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PROSITE; PS01299;
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ALDEHYDE_DEHYDR_GLU;
                                                                                                                           Neognathae;
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35913 MW;
                                                                                                                                                                 Chordata;
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Pred. No. 6.1e-
30; Mismatches
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4BB0FA39D4C22DCD CRC64;
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Galliformes; Phasian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update) annotation updat
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                                                                                                                              cebrata; Euteleostomi;
Phasianidae; Phasiani
                                                                                                                                                                                                                                                          update)
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ephrin-B ligands.";
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; Pipidae;
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Query Match
Best Local Similarity
Matches 141; Conserv
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Best Local :
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                                              MEDLINE=21290827; PubMed=11397014;
Chan J., Mably J.D., Serluca F.C., Chen J
Thomas M.C., Cleary J.A., Brennan C., Fis
"Morphogenesis of prechordal plate and no
eph/ephrin b signaling.";
Dev. Biol. 234:470-482(2001).
EMBL, AF375224, AAK64274.1;
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; UNKNOWN 1.
SEQUENCE 341 AA, 37849 MW; CB522F20E0
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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SEQUENCE
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SIGNAL
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"Coding sequence of chicken ephrin-B2.";
Submitted (AUG-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF180729; AAD53948.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
ProDom; PD00523; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                        Ephrin B1
                                                                                                                                                                                                                                                                                                                                                      Q90Z33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOYEYYKVYMVDKDÓADSCAIRKDNTPLLNCAKPDÓDVKFTIKFÓEFSPNLWGLEFQKNK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALMVLWRTALAKSIVLDPIYWNSSNPKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
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333 AA;
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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333 E.
; 36761 MW;
          33.3%;
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20,
  49;
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 Score 616; DB
Pred. No. 1.3e-
49; Mismatches
                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.1
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EPHRIN-B2.
; 4C28E8CB211B7783 CRC64;
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                                                CB922F20E0D93E94
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                                                                                                                                                             Chen J.N., Goldstein N.B.
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                                                                                                                                                  notochord requires
             DB 13;
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                                                  CRC64;
                       Length 341;
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  38;
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 Gaps
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                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q90Z32;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                            Chan J., Mably J.D., Serluca P.C., Chen J.N., Goldstein N.B., Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M. "Morphogenesis of prechordal plate and notochord requires intact eph/ephrin b signaling.", eph/ephrin b signaling.", Berusa J. 34:470-482 (2001).

EMBL, AF375236; ARK64276.1; -.

InterPro, IPR001799; Ephrin.
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephrin B2b
                                                                                                                                                                                                                                                                                   Pfam; PF00812; Ephrin;
ProDom; PD002533; Ephri
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21290827;
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201
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                                                                                                                                                                           30 LEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQG
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QIDSMQNGESGGKSG-
                        --DPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                             SLQGGVCLTRGMKVLLRVGQSPRGGAV----PRKPVSEMPMERDRGAAHSLEPGKENLPG
                                                                                                         ETCHVTKSDMLLLNCDKPDQDVKFTFKFQEFSPNLWGLEFLRGKDYHIISTSNSTFEGLD
                                                                                                                             RRCEAPPAPULLLTCDRPDLDLRFTIKFQEYSPULWGHEFRSHHDYYIIATSDGTREGLE
                                                                                                                                                      LESIYWNTSNTKFVPGRGVVLYPQIGDXMDIVCPRIK-PGSTEQTNIEYFRVYLVPKEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQEGLENREGGVCSTRSMKIIMKVGQDPNAPDPDLPDLPDRPYDNEIKDPTTSPSRKTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYL
                                                   NHHGGVCRSKSMKLVLRVGQSPTDSFSAKNHPTRNPPKYPENKDQNTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                      Ephrin; 1.
; 36998 MW;
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41.0%;
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-ESVGSAGSDVALFAGV--ASGAVIFILIIIALVALLH
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Last annotation updat
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; Craniata; Veri
Teleostei; Osta
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                                                                                                                                                                                                                               Score 605.5; DB 1
Pred. No. 7.9e-39;
                                                                                                                                                                                                                                                                      341497E0FE9473BD CRC64;
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250
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RESULT 7
2996H9
ID 0996
AC 099
RESULT
Q9U3M2
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
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                                                                                                                                                                       문
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Best Local S
Matches 84
              Q9U3M2;
Q9U3M2;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephrin-B2 (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Ver
Amphibia, Batrachia, Anura, Mesobatrachia,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDILINE=97411149; PubMed=9259557;

MEDILINE=97411149; PubMed=9259557;

Smith A., Robinson V., Patel K., Wilkinson D.G.;

"The EphA4 and EphB1 receptor tyrosine kinases as regulate targeted migration of branchial neural (Curr. Biol. 7:561-570(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
   C43F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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ProDom; PD002533; Ephrin; 1.
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EMBL; AF128844; AAD32610:1; -.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                128
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                                                                                                                                                                   IIPLR---TAEGVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                         GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLG------GGGGMGPREAEPGEL
                                                                                                                                                                                                                                                                                                        ESGTNGKSSTTSPHVNGPEGSSTEGKNAGHSSILGSEVAL-----FAGIASGSIIFIV
                                                                                                                                                                                                                                                                                                                                                                            EFQRDXDYYIISTSNGSLEGVDNQEGGVCVTKAMXILMKVGQDPNFHNHRGASSTRRPDH
                                                                                                                                                                                                                                                                                                                                                                                                            EFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSP----RGGAVPRKPVS 182
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                (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 21,
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                                                                                   PRELIMINARY;
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5
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Pred. No. 1.2e
35; Mismatches
                Created)
Last sequences
Last anno
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Last
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                sequence update)
annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
.2e-18;
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                update)
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crest cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligands.";
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Query Match
Best Local
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Q9U474;
01-MAY-2000
01-MAY-2000
01-DEC-2001
"Genome sequence of the nematode investigating biology. The C. elescience 282:2012-2018(1998).
                                                                SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.

Chromadorea; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                            VAB-2 (Hypothetical VAB-2 OR Y37E11AR.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
ProDom; PB002533; Ephrin; 1.
SEQUENCE 237 AA; 26748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                   epidermal morphogenesis
Cell 99:781-790(1999).
                                                                                                                                                                 Chisholm A.D.;
"The ephrin VAB-2/EFN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Mortimore B.J.;
                                                                                                                                                                                                    Chin-Sang I.D.,
                                                                                                                                                                                                                        MEDLINE=20084449;
                                                                                                                                                                                                                                          STRAIN=N2
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
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MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRRGIENPK--FAARTLKKDRDAEHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTDHVISVHIGDRVSIRCPKSDET 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEVGQ
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10 (TrEMBLrel. 13,
11 (TrEMBLrel. 19,
11 thetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                    George
                                                                                                                                                                                                    PubMed=10619431;
eorge S.E., Ding M.,
                                                                   PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9851916;
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25.7%;
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in C. elegans.";
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Last annotation update)
Y37E11AR.6).
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Pred. No. 6.1e.
41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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              ode C. elegans: a platform elegans Sequencing Consort
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                                                                                                                                                                                                     Moseley S.L.,
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                                                                                                                                                                                                                                                                                                                             Rhabditida; Rhabditoidea;
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                  Consortium.
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                                                                                                                                                                                                       Lynch A.S.,
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Best Local S
Matches 64
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"Direct Submission.";
Submitted (JUL-2001) to the EMBL
EMBL; AF201079; AAF25647.1; -.
EMBL; AF004759; AAF88436.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF000812; Ebhrin; 1.
ProDom; PD002553; Ephrin; 1.
SEQUENCE 279 AA; 32068 MW; E
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Q9V4E1;
01-MAY-2000
MEDINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Bahlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Dai Y., Kunes S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota, Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN OR CG1862.
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01-OCT-2000 (TremBlrel.
01-JUN-2001 (TremBlrel.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BERKELEY;
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Miller N., Maggi L.;
"The sequence of C. elegans cosmid Y37E11AR.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIVCPFF - - - DENSDELTEQSIIYRVTEEEYENCERRSKAKELGRCTQPYQEEKLKVAFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DIGPHHHRHHHKKTTTTTTTSTSTS-----TPKTIPPV
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15,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
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Pred. No. 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ephrin.";
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.F.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Lin M., Kallush F., Karpen G.H., Ke Z., Kenn-Hs., Ibegwam C.,
Valush F., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Matted B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Stapleton M., Stupski M.P., Shinh T.,
RA Syle B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syle B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syle B.C., Schen H., Wang A.H., Wang X.H., Wang X.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yel J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yel J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Sheng X.H., Zhong F.N., Robin G.M., Venter J.C.,
RA Sheng X.H., Zhong F.N., Rabin G.M., Venter J.C.,
RA Sheng X.H., Zhong F.N., Rabin G.M., Venter J.C.,
RA Sheng X.H., Zhong F.N., Rabin G.M., Venter J.C.,
RA Sheng S.H., Sheng M.S., Sheng M.S., Shen
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ProDom; PD002533; Ephrin; 1.
SEQUENCE 652 AA; 72302 MW;
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InterPro; IPR001799; Ephrin.
                                                               548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 VYWNSANKRFQAEG-GYVLYPQIG-----DRLDLLCPRARPPGPHSSPNYEFYKLYLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                             PNEVVKNESLTYNSGAATSDGNIF
                                                                                                    PVYIVQD-----
                                                                                                                                                                                   MGPREAEPG----ELGIALRG-----
                                                                                                                                                                                                                                                                                                    HVNSHGNNIAIGINIGINGGQIIGGPQSAGIPINPLSGNNNINGIPTTINSNIDQFNRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSL-----EPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQPNIIGNHVGTNAVGTGIVGGGGIIL--
                                                                                                                                                                                                                                                                 SMPAVAGAAGGLALLILIGVAGAGGAMCWRRRRAKPSESRHPGPG-SFGRGGSLGLGGGGG
                                                                                                                                         NG----AYPGHHHIQTGIRINNVPTQHNYPSHKGNANSNINGNDDH----HHYNK-
                                                                                                                                                                                                                                                                                                                                                  KENLPGDPTSNATSRGAEG-----PLPP-----
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Similarity 22.9%;
88; Conservative 5
                                                                                                    GPPQSPPNIY
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Pred. No. 6.1e-06;
0; Mismatches 136
                                                                                                    337
                                                               571
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                                                                                                                                                                                   ---GGAADPPFCPHYEKVSGDYGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136;
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Q98TZ1 ID Q AC Q

Q98TZ1;

PRELIMINARY;

PRT;

202 AA

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RESULT 12
Q9D7K8
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EP SEQUENCE FROM N.A.

EN SAITON N.A.

EN SCHIML L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

EN Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

EN Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

EN Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

EN Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

EN SAKAI K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Cres O1-JUN-2001 (TrEMBLrel. 17, Last O1-OCT-2001 (TrEMBLrel. 18, Last Ephrin-A6 (Fragment).
Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata; C.
                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310004J15, full insert sequence.
                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                      EFNA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Menzel P., Valencia F., (
"Ephrin-A6, a new ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSTIE; PS01299; EPHRIN; 1.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system."
                                                                                                                                                                                                               NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                Q9D7K8;
                                                                                                                                                                                                                                                                                                                                                                                               Q9D7K8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF317286; AAK00944.1;
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNATSRGAEGPLPPPSMPAVAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SETPGAFKRWECNKPPAPFVPVRFSEKIQRFTPFSLGFEFRPGETYYYISVPTPGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAPPAPHLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT-SDGTREGL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 27.!
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGRCLKLRVSVCCR
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Last sequence Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178.5; DE
Pred. No. 3e-06;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91E2716FF91353F9 CRC64;
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A receptors in the
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visual
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RESULT 13
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RX MEDINE-C57BL/GJ; TISSUE=EMBRYO;

RX MARDINE-C1085660; PubMed-11217851;

RA MARINE-2108560; PubMed-11217851;

RA Alawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Alawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alawa T., Salto R.,

RA Alawa T., Salto R.,

RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Wishido I., Pesole G., Quackenbush J.,

RA Kadota K., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kahl P., Lewis S., Mareuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Sanida M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Jyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Mordone P., Ring B., Ringwald M., Rodriguez I., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Ma
Best Loc
Matches
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Q9CZS8;
Q9CZS8;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; EPHRIN; 1.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS00678; WD REPEATS 1;
SEQUENCE 205 AA; 23772 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AKO09144, BAB26102.1;
MGD; MGI:103236; Efnal.
InterPro; IPR001799; Ephrin.
InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK009144; BAB26102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSVKFQRFTPFILGKEFKEGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGVIGIVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.0%;
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Pred. No. 2.3e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; 1
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E37E55767459A4EC CRC64;
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76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
                                                     K. -F.,
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RESULT
Q9N178
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                                                                                      Query Match
Best Local S
Matches 106
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Best Local S
Matches 61
                                                                                                                                                                                                                     Mamm. Genome 11:1087'1092(2000).

EMBL; AF222861; AAF37271.1; -.

InterPro; IPR001073; C1q.

InterPro; IPR000087; Collagen.

Pfam; PF01391; Collagen; 8.

PRINTS; PR00007; COMPLEMNTC1Q.

PRODOM; PD000007; COLlagen; 2.

SMART; SM00110; C1Q; 1.

PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9N178;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                 Collagen.
SEQUENCE
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PRINTS; PR01347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
SEQUENCE 206 AA; 22859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21015405; PubMed=11130976;
Nielsen V.H., Bendixen C., Arnbjerg
Shukri N.M., Thomsen B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9N178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki
"Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abnormal growth plate function in pigs carrying a dominant in type X collagen.";
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  212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGESGTSGWRGGHAPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEAPPAPNL-LLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG 147
    MGPP-
                                        MGPPHSGPGGYRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQI-GDR-L 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAH-SLEPGKENLPG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAEGANSFORWNCSMPFAPFSPVRFSEKIORYTPFPLGFEFLPGETYYYISVPTPESPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIYWNSSNPRL-LRGDAVVELGFNDYLDIFCPHYESPGPPEGP--ETFALYIVDWSGYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 8.8%; So
Similarity 28.1%; Pr
61; Conservative 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
    -GPPGV--
                                                                                                                                                                                 675
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                                                                                    8.4%; Score 156; DB 6; llarity 28.6%; Pred. No. 0.00063; Conservative 17; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                               AA;
                                                                                                                                                                                 65447 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15,
15,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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Pred. No. 4.3e-
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                 26397B10310383F9
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-GKR--GENGFPGQPGIKGDRGF 240
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Sus.
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01-NOV-1998
01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01347; EPHRIN.

Prodom; PD002533; Ephrin; 1.

PROSITE; PS01299; EPHRIN; 1.

PROSITE; PS00290; IG MHC; UNKNOWN 1.

SEQUENCE 229 AA; \( \overline{Z} \) 6115 MW; 86\(\overline{B} \) 4462F67AF6F5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001799; Ephrin.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00812; Ephrin; I.
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"Eph signalling is required for 
the somites.";
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                            33 VYWNSANKREQAEGGYVLYPQIGDRIDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC
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  PLHHHGQECLRLKVDVV-----GPHGSKNKKKMVEKVEEIEGKMAAGGVHNPSNRLPADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPGPVGPAGAKGVPGHNGEAGPRGAPGIPGTRGPIGPPGIPGFPGSKGDPGNP---
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                                                 SL--QGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP
                                                                                                         KPHSFDQLRWECSRPFAPHAPEKFSEKFQRFTPFTLGKEFRQGESYYYIS-----K
                                                                                                                                                     EAPPAPNLLLTCDR----POLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE
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Last annotation update)
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Pred. No. 0.00022;
3; Mismatches 93;
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MEDIINE=20536494; PubMed=10965041;

Saito K., Naito I., Seki T., Oohashi T., Kimu Kishiro Y., Sado Y., Yoshioka H., Ninomiya Y.

"Differential Expression of Mouse a5(IV) and Epithelial Basement Membranes.";

J. Biochem. 128:427-434(2000).

EMBL; AB041350; BAB13673.1; -.
Q9IB91;
01-0CT-2000 (TrEMBLrel. 15, C
01-0CT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, I
Tyme I collagen alpha 1.
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Collagen.
SEQUENCE
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01-MAR-2001 (TrimBirel. 16, Last sequence update)
01-JUN-2002 (TrimBirel. 21, Last annotation update)
Type IV collagen alpha 5 chain.
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InterPro; IPR000087; Collagen.
InterPro; IPR001442; ProcollagnC4.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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; PD003923; ProcollagnC4;
SM00111; C4; 2.
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86; Conserv
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                                        Created)
Last sequence update)
Last annotation updat
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Pred. No. 0.0
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Lya Y.;
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Matches 86
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O17JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation updat
"""" hetical 31.6 kDa protein.
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Collagen.
SEQUENCE 1447 AA.
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"Expression and characterization of Kenopus type I colla
(COLLAI) during embryonic development.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB034701; BA94972.1; -
InterPro; IPR000085; Follagen
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001087; VMF_C.
             SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1021
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ProDom; PD002078; Fib collagen C;
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
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Pfam; PF01391; Collagen; 18.
Pfam; PF00093; vwc; 1.
                                                                                                                                            Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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                                                                                                       NCBI_TaxID=6239;
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                  PubMed=9851916;
                                                                                                                                                                        Nematoda;
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Pred. No. 0.00
13; Mismatches
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Best Local &
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Submitted (JTL-2001) to the EMBL/GenBank/DDBJ da
EMBL; AF022385; AAB69961.1; -.
InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col_cuticle_N.
Pfam; PF01391; Collagen; 3.
Pfam; PF01494; Col_cuticle_N; 1.
Hypothetical proteIn.
SEQUENCE 325 AA; 31591 MW; 6538D4E37C9EC202
                                                                                                                                                                                          Q17208;
01.NOV-1996 (TrEMBLrel. 01,
01.NOV-1996 (TrEMBLrel. 01,
01.JUN-2002 (TrEMBLrel. 21,
Collagen (Fragment).
                                                                                                          Bombyz mori (Šilk moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
NCBI TaxID=7091;
SEQUENCE FROM N.A.
STRAIN=EUROPEAN 200X300; TISSUB=IMAGINAL WING DISC;
MEDLINE=97148965; PubMed=8995790;
MEDLINE=97148965; PubMed=8995790;
Chareyre P.P., Besson M.M., Fourche J.J., Bosquet G.G.;
"Identification of a Bombyx collagenous protein with multiple domains of Gly-Xaa-Yaa repeats: cDNA characterization and regu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pauley A., Gattung S.;
"The sequence of C. elegans
Submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  μ
                                                                                                                                                                                                                                                                                                                                                              PGP-AGGPGQPG---HSGGAGSPGPQGP----PGPSGQPGHSGNDGVPGAPGN
                                                                                                                                                                                                                                                                                                                                                                                                 -GPREAEPGELGIALRGGGAADP-PFCPHYEKVSGDYGHPVYIVQDGPPQSPPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GDAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTTRPSSGSS------FLLGRNKRQAQCNCGAQSRGCPAGPPGP------96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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Last annotation updat
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EMBL/GenBank/DDBJ databases.
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Pred. No. 0.00095;
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Best Local Similarity
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Q19111;
01-NOV-1996
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SEQUENCE
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 282:2012-2018(1998).
EMBL; Z67990; CAA91932.1; -.
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01-JUN-2002
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InterPro; IPR001419; Glutenin.
Pfam; PF01391; Collagen; 5.
PRINTS; PR00210; GLUTENIN.
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                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col cuticle_N.
Pfam; PP01391; Collagen; 2.
Pfam; PP01484; Coll cuticle_N; 1.
SEQUENCE 316 AA; 29444 MW; 4D76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99069613;
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Insect Biochem. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                          276
                                                                                                                                                                              144
                                                                                                                                                                                                                        168 GOSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nvestigating biology
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  GSGSAGGPGPKGPPGPAGQPGSDGNPGTAGPPGNPGGEGEKGICPKYCAIDG
                                       GLGGGGGMGPR-----
                                                                                  PGPAGPPGNDGQPGQPGGPG--QDGASSAGG
                                                                                                                                                                           GASGKGAAAPCEPSTPPPCQ-PCPAGPPGPPGPPGEPGGPGGPGPAGSPAGPSGPGPAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPREAEPGELGIALRG----GGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
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                                                                                                                                 EGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP-GSPGRGGSL
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49; Conserv
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(NOV-1995)
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                                                                                                                                                                                                                                                                     12;
                                          EAEPGELGIALRGGGAADPPFCPHYEKVSG
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Last annotation update)
                                                                                                                                                                                                                                                                Score 148.5; |
Pred. No. 0.00
12; Mismatches
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Pred. No. 0.00
14; Mismatches
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                                                                                       ----EAGPGPAGPPGPAGPAGPDGQS
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RESULT 22
Q91718
ID Q9171
AC Q9171
DT 01-NC
DT 01-NC
DT 01-JU
DE Alpha
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abe N. Muragaki Y., Yoshioka H., Inoue H., Ninomiya Y., "Identification of a novel collagen chain represented by interruptions in the triple-helical region."; Cell. Mol. Biol. Res. 196:576-582 (1993).

EMBL, D17546; BAA04483.1; -.

EMBL, D17546; BAA04483.1; -.

MGD; MGI:8849; Collagen.

InterPro; IPR000087; Collagen.

InterPro; IPR003129; TSPN.

Pfam; PF01391; Collagen; 8.

Pfam; PF01391; TSPN; 1.
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Q61434;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                   Q91718;
Q91718;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
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Mammalia; Eutheria; Rodentia;
MCBI TaxID=10090;
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    Alpha-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPPHSGPGGVRVGALLLLGVLG-LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                                                                                                                                                                              DDMEGS-GIPLWTTARSSDGLQGPPGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --PGAQGPPGPQGPPGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCPRAR-PPGPHSSPNYEFYKLYLVGGAQGRRCE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPP--GPAGPQ-----GPAGPVVQSPNSQPV
                                                                                                                                                                                                                                                                         EKVSGDYGHPVYIVQ-----DGPPQSP
                                                                                                                                                                                                                                                                                                                                                                 RAKPSESRHPGP-GSFGRGGSLGLGGGGGGGGPREAEPGELGIALRGG--GAADPPFCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGKENLPGDPTSNATSRGAEGP--LP-PPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSGFSGDIESLRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKP--VSEMPMERDR-GAAHSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKGEKGDPGIGPRGPPGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----APPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT
                                                                                                                                                                                                                                                                                                                                                                                                            PGPAGLPGVP-----GKEGPPGFPGPPGPPGPPGKEGP----PGVAGQKGSV----
type
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                                                                                                                                                                                                                                                                                                                      -GDVGIPGPKGSKGDLGPIGMPGKSGLA--
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6 (TrEMBLrel.
2 (TrEMBLrel.
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5 (TrEMBLrel. 01, 05 (TrEMBLrel. 01, 12 (TrEMBLrel. 21, 12 (TrEMBLrel. 21, 15 ) oe II' collagen.
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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23.7%;
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21,
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Last
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                                                                  Created)
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Pred. No. 0.0
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                          sequence update) annotation updat
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                                                                                                                                                                                                                                440
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on update)
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                          update)
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DT 011

CGN MCCG

GGN CGGN

CGGN MG

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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01410; COLFI; 1.
Pfam; PF0139; Collagen; 18.
Pfam; PF00093; vvc; 1.
ProDom; PD000007; Collagen; 3.
ProDom; PD002078; Fib collagen_C; 1
SWART; SW00038; COLFI; 1.
SWART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; |
Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q62001 PRELIMINARY; PRT; 1774 AA. Q62001; Q65072; Q62001. Q660672; O1-NOV-1996 (TERMBLrel. 01, Created) O1-NOV-1996 (TERMBLrel. 01, Last sequence update) O1-JUN-2002 (TERMBLrel. 21, Last annotation update) Procollagen, type XVIII, alpha 1 precursor (XVIII) (Procollagen, type XVIII, alpha 1) (Alpha-1 type XVIII)
                                                                                                                         alpha
chain.
                                                                                                                                        TISSUE=PRIMARY TAIL CULTURE;

MEDLINE=94245707; PubMed=8188673;

Rehn M., Hintikka E., Pihlajaniemi T.;

"Primary structure of the alpha 1 chain of mouse type XVIII collagen,

partial structure of the corresponding gene, and comparison of the
alpha 1(XVIII) chain with its homologue, the alpha 1(XV) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Su M.W., Suzuki H.R., Bieker J.J., Solursh M., Ramirez F., "Expression of two nonallelic type II procollagen genes du laevis embryogenesis is characterized by stage-specific prolaternatively spliced transcripts.";
J. Cell Biol. 115:565-575(1991).
EMBL, M63596, AAA49679.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphila; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI TaxID=8355;
[1]
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=92011898;
                          SEQUENCE OF 1-562 FROM N.A. MEDLINE=94240112; PubMed=8183894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VMF_C.
                                                                                                    J. Biol.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGGLALLLLG--VAGAGGAMCWRRR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01208;
     Pihlajaniemi
                                                                                                    Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                    269:13929-13935(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1918153;
                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
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31.1%;
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Pred. No. 0.00
L1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43026FFF08FB0314 CRC64;
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80;
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                                                                                                                                                                                                                                                                                                                                                                              Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XVIII
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VIII collagen)
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     during Xenopus production of
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                                                                                                                                                                                                                                                                                                                                                                                Mus.
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J. Biol. Chem. 270:4705-4711(1995)
EMBL; U03715; AACS2903.1; JOINED.
EMBL; U03716; AACS2903.1; JOINED.
EMBL; U04716; AACS2903.1; JOINED.
EMBL; U34607; AACS2903.1; JOINED.
EMBL; U34608; AACS2903.1; JOINED.
EMBL; U34609; AACS2903.1; JOINED.
EMBL; U34610; AACS2903.1; JOINED.
EMBL; U34610; AACS2903.1; JOINED.
EMBL; U34611; AACS2903.1; JOINED.
EMBL; U34612; AACS2903.1; JOINED.
EMBL; U34613; AACS2903.1; JOINED.
EMBL; U34614; AACS2903.1; JOINED.
EMBL; U34615; AACS2903.1; JOINED.
EMBL; U34617; AACS2903.1; JOINED.
EMBL; U34618; AACS2903.1; JOINED.
EMBL; U34619; AACS2903.1; JOINED.
EMBL; U34611; AACS2903.1; JOINED.
EMBL; U34612; AACS2903.1; JOINED.
EMBL; U34613; AACS2903.1; JOINED.
EMBL; U34613; AACS2903.1; JOINED.
EMBL; U34613; AACS2903.1; JOINED.
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Pfam; PF01392; Fz; 1.
Pfam; PF02210; TSPN; 1.
ProDom; PD000007; Collagen; 1
SWART; SW00282; LamG; 1.
SWART; SW00282; LamG; 1.
SWART; SM00210; TSPN; 1.
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SEQUENCE
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"Identification of three N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and tissue-specific differences in the transcripts. The longest form contains and Drosophila frizzled proteins.", J. Biol. Chem. 270:4705-4711(1995).
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                                1048
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PROSITE; PS50038; FZ; 1.
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InterPro; IPR000024; Fz. domain.
InterPro; IPR001791; Laminin_G.
InterPro; IPR003129; TSPN.
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MEDLINE=95181468; PubMed=78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  872
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                                                                                          312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPHSGPGGVRVGALLLLGVLG-LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                DDMEGS-GIPLWTTARSSDGLQGPPGSP
                                                                                      EKVSGDYGHPVYIVQ-----DGPPQSP
                                                                                                                                                                                                             RAKPSESRHPGP-GSFGRGGSLGLGGGGGGGGREAEPGELGIALRGG--GAADPPFCPHY
                                                                                                                                                                                                                                                                          PGPAGLPGVP-----GKEGPPGFPGPPGPPGPPGKEGP-----PGVAGQKGSV-----
                                                                                                                                                                                                                                                                                                                                 PGKENLPGDPTSNATSRGAEGP--LP-PPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRR
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1. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1774 AA;
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                                                                                                                                                                                SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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Collagen; Signal.
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675 AA;
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675 C
63069 MW;
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Rodentia;
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Q90800;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-UUN-2002 (TrEMBLrel. 21, Last anno
Collagen-alpha-3 type IX precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Cranjat
TISSUE-KINNEY;
MEDLINE=20005934; PubMed=10534397;
MEDLINE=20005934; PubMed=10534397;
Lu W., Phillips C.L., Killen P.D., Hlaing T., Harrison Lu W., Phillips C.L., Killen P.D., Haing T., Harrison Elder F.F.B., Miner J.H., Overbeek P.A., Meisler M.H.;
"Insertional mutation of the collagen genes col4a3 and model of alport syndrome.";
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MEDLINE=92241276; PubMed=1572350;

Brewton R.G., Ouspenskaia M.V., van der Rest M., Mayne R.;

"Cloning of the chicken alpha 3(IX) collagen chain complet primary structure of type IX collagen.";

Dischem. 205:443-449(1992).
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Aves; Neognathae; Galliformes; Phasianidae;
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COLLAGEN-ALPHA-3 TYPE IX.
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Pred. No. 0.
                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local
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EMBL, AF169387, AAD50449.1; -.

MGD; MGI:104688; Col4a3

InterPro; IPR000087; Collagen.

InterPro; IPR001442; ProcollagnC4.

InterPro; IPR000504; RNA_rec_mot.

Pfam; PF01413; C4; 2.

Pfam; PF01391; Collagen; 21.

ProDom; PD003007; Collagen; 6.

ProDom; PD00303; ProcollagnC4; 1.

SMART; SM00111; C4; 2.
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SEQUENCE
  "Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998).
EMBL; Z81503; CAB04111.1; -.
                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
F14F7.1 protein.
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                                                                                                                     SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                    McMurray
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             017805
                                                                                                   none ;
                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                    F14F7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGAPGSPGSPGHPGKPGPAGDLGL----KGQKGFPGPPG-----STGPPGPPG
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97; Conserv
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                                                                                                                                                                                                       A.A.;
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                                                                                                                       PubMed=9851916;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                           EMBL/GenBank/DDBJ
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Pred. No. 0
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RESULT 27
Q94620
                                                                                               AC CONTRACTOR REPRESENTATION OF THE PROPERTY O
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Best Local S
Matches 83
Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q94620;
Q94620;
                                                                                                                                                                                                        Wang T., Deom C.M., Hussey R.S.;
"Identification of a Meloidogyne incognita cuticle collagen gene ar
characterization of the developmental expression of three collagen
genes in parasitic stages.";
Mol. Biochem. Parasitol. 93:131-134(1998).
EMBL; U68729; AAC48358.1;
InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col cuticle N.
Defam. Defan191. Collagen.
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InterPro; IPR002486; Col cuticle N.
Pfam; PF01484; Col cuticle N; 1.
SEQUENCE 305 AA; 29497 NW; 161BFA90D024C2E6 CRC64;
                                                                                                                         Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meloidogyne incognita (southern root-knot nematode).
Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, T
Enchoidea, Heteroderidae, Meloidogyninae, Meloidogyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98324411;
Wang T., Deom C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cuticle preprocollagen.
                                                                                                                                                               Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
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80
  7.9%;
ilarity 28.4%;
Conservative 1
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                                                                                               AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9662034;
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29361 MW;
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  ; Score 145.5; DB 5; ; Pred. No. 0.0017; 14; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                           COLLAGEN
                                                                                               825AEF0249FDFC78 CRC64;
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Matches 87
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Schrimi I., Batlancelli R., Barsh G.,
Ra Schai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carminci P., de Bonaldo M.F.,
Ra Blake J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
Ra Blake J., Balt C., Fletcher C., Fujita M., Gariboldi M.,
Ra Blake J., Balt D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Blake J., Balt C., Humann M., Hume D.A., Kamiya M., Lee N.H.,
Ra Brownstein M.J., Balt C., Maszarelli J., Mombaerts P.,
Ra Brownstein M.J., Balt C., Walmann M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,
Ra Brownstein M., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,
Ra Brownstein M., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,
Ra Brownstein M., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,
Ra Brownstein M., Schoenbach C., Seya T., Shibate Y., Storch K.,
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SEQUENCE
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Q9D0D2;
01-JUN-2001
01-JUN-2001
01-JUN-2002
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Pfam; PF01391; Collagen; 11.
PRINTS; PR01582; KV33CHANNEL.
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STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
EMBL; AK011547; BAB27690.1; -.
MGD; MGI:88465; Col9a1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                              FQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLLRVGQSPRGG
                                                                                                   CPNSCPPGRSGYPG-----LPGMRGHKGAKGEIGE-----
                                                                                                                                                              CPRARPPGPHSSPNYEFYKLYLVG-----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIK 116
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1 (TrEMBLrel. 17,
2 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 145; DB 11; Length 680; llarity 24.0%; Pred. No. 0.0045; Conservative 22; Mismatches 131; Indels 12
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pfam; pF01410; COLFI; 1...
pfam; pF01291; COLPagen; 17.
pfam; pF02210; TSPN; 1...
probom; pD000007; Collagen; 3.
probom; pD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00285; LamG; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
SEQUENCE 1745 AA; 172051 MW; 58
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Q9NZQ6;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
COllagen type V alpha 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PLACENTA, AND HEART;
MEDLLINE=20187594; PubMede10722718;
Imamura Y., Scott I.C., Greenspan D.S.;
"The pro-alpha3 (V) collagen chain. Compexpression domains in adult and develop the structures and expression domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        procollagen chains.";
J. Biol. Chem. 275:8749-8759(2000).
EMBL; AF177941; AAF59902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000087; Collagen.
InterPro; IPR0010885; Fib_collagen_C.
InterPro; IPR001791; Laminin_G.
InterPro; IPR003129; TSPN.
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                                                                                                                                                                                                                                                                                          884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 EP 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 MPAVAGAAG-----GLALL--LLGVAGAGGAMCWRRRRAKPSE-----SRHPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 GIPGAAGDQGQRGPPGETGPEGDRGI-----QGSRGIPGSPGPKGDTGLPGVDGRDGIPG
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                                                                                                TIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRG
                                                                                                                                                                                                                        LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCE-----APPAPNLLLTCDRPDLDLRF
                                                                                                                                                                                                                                                                                      GPPGHQGKDG-RPGHPGQRGELG------FQGQTG----
                                                                                                                                                                                                                                                                                                                                                    GPP-HSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - PGSFGRGGSLGL-GGGGGMGPREAE--PGELGIALRGG--GAADPPFCPHYEKVSGDYG
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                                                                                                                                                                                                                                                                                                                                                                                                                  , 88
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 145; 24.0%; Pred. No. 0.
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15, La
21, La
chain.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5E8FF97135397AC1 CRC64;
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                                     --- EQGLPGLEG-----
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0.013;
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Matches
                                                                                               Q96QB3 PRELIMINARY;
Q96QB3;
Q1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-JUN-2002 (TrEMBLrel. 21, L
Type V preprocollagen alpha 2
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cuticle collagen gene.";

Mol. Biochem. Parasitol. 83:121-124(1996).

EMBL; U40766; AAC47437.1; -.

InterPro; IPR000087; Collagen.

InterPro; IPR002486; Col_cuticle_N.

Pfam; PF01391; Collagen; 2.

Pfam; PF01484; Col_cuticle_N; 1.

SEQUENCE 309 AA; 29472 MW; 0C6C9D5BA76C8916 CRC64;
                                                                                Type V
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Q25466;
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     Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97164124; PubMed=9010847; Ray C., Wang T.Y., Hussey R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meloidogyne incognita (southern root-knot nematode).
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
NCBI_TaxID=6306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
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                                                                                                                                                                                                                                                                                                                                             QPGG----
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5 (TrEMBLrel. 01,
1 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                -PGQPGSPA-QSQEAGPAPPGPPGDAGAPGQPGNPGPAGQPGGPGGPGP
                                                                                                                                                                                                                                                                                                                                                                                              EAEPGELGIALRGGGAADPPFCPHYEKVSG
       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%;
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                                                                                                  Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 144.5; |
Pred. No. 0.00
L4; Mismatches
          Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence up
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          Hominidae;
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                                                                                                                                                                                                                                                                                                                                                  298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
          Euteleostomi; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GPAGPPGSPGAPG
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       RESULT 32

Q90W37

ID Q90W3

AC Q90W3

AC Q90W3

DT 01-DE

DT 01-JU

DE Alpha

GN COL2AA

OS Gallu

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OC Archar

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Best Local
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EMBL; AY016295; AALI3166.1; JOINED EMBL; AY016295; AALI3166.1; JOINED EMBL; AY016291; AALI3166.1; JOINED EMBL; AY016292; AALI3166.1; JOINED EMBL; AY016292; AALI3166.1; JOINED EMBL; AY016292; AALI3166.1; JOINED EMBL; AY016293; AALI3166.1; JOINED EMBL; AY016294; AALI3166.1; JOINED EMBL; AY016294; AALI3166.1; JOINED InterPro; IPR000887; Collagen.

InterPro; IPR000885; Fib collagen_C. Pfam; PF01391; Collagen; 18. ProDom; PD000007; Collagen; 6. ProDom; PD000007; Collagen; 6. ProDom; PD0000078; Fib collagen_C; 1.
Caixia X., Yongzhi X., Siqi G., Yiying Submitted (JUL-2001) to the EMBL/GenBa: EMBL; AY046949; AAK98621.1; -. InterPro; IPR000087; Collagen. InterPro; IPR000085; Fib_collagen_C. Pfam; PF01391; Collagen; 18. ProDom; PD00007; Collagen; 6. ProDom; PD002078; Fib_collagen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                         Q90W37
Q90W37;
Q90W37;
Q1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 21, L
01-JUN-2002 (TrEMBLrel. 21, L
Alpha 1 type IIA collagen pre
COL2A1.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Archosauria; Aves; l
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002078;
Collagen.
NON_TER 1
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                      TISSUE-STERNAL,
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21451029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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oniemi M., Kvist
                                                                                                                                                                                                                                                                                                                                             ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7,8%;
33.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                             G., Yiying S.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 144.5; I
Pred. No. 0.01:
12; Mismatches
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collagen genes.";
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SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.

Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Streptomycetaceae; Streptomyces.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SCO5128.
SCO5128 OR SC9E12.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model coelicor A3(2).";
Nature 417:141-147(2002).
EMBL; AL391751; CAC05758.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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                                                 LTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGM 161
                                                                                                                                                                                                                                                                        PPHSGPG------GVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAMCWRRRRAKPSESRHPG-PGSFGRGGSLGLGGGGGGGGREAEPGELGIALRGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- DRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAG 246
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                                                                                                                                                              YPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQ-----GRRCEA---PPAPNLL 101
                                                                                                                                                                                                                   PRKSGPGKGTQGGGSTNGAGLPAGSAPTAGTPGAAGARGAGPAGASGAG------
                                                                                                                                                                                                                                                                                                                                                             Similarity
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23.5%;
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28.1%;
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134999
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                                                                                                                                                                                                                                                                                                                                23; Mismatches 130;
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                                                                                                                                                                                                                                                                                                                                                       Score 143.5; DB 16; Pred. No. 0.0068;
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W; 88D9AAB17F214FF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                            E5032698A20A0711 CRC64;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00111; C4; 2.
Collagen.
SEQUENCE 1747 AA; 1:
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J. Biol. Chem. 269:33167-3171(1994).

EMBL; X76730; CAA54146.1; -.

InterPro; IPR000087; Collagen.

InterPro; IPR001442; ProcollagnC4.
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01-NOV-1996 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
Alpha2(IV)-like collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF01413; C4; 2.
Pfam, PF01391; Collagen; 21.
ProDom; PD000007; Collagen; 6.
ProDom; PD003923; ProcollagnC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q26640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a cell lineage-specific urchin .alpha.2(IV)-like collagen chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exposito J.Y., Suzuki H., Geourjon C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94230414; PubMed=8175744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                 GGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLGLGGGGGMGP
                                                                                                                                                                                                                                                                                                                                                          PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG
                                                                                                                                                                                                                                                                                                                                                                                                                GPRGMDG----MKGATGEVGDLGSYGDYGEKGLPGYSGERGFPGNPGIPGLLGMNGEKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPGGVRVGALLLLGVLGLVSGLSLBPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TaxID=7668
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G----FMGQKGGRGP----PGRÅGPAGPARSGNQSFQGFPGDTGNTGLKGMRGIQGALG
                                                                                                                                                   EMPMERDRGAAHSLEPGKENLPGDP----TSNATSRGAEGPL----PPPSMPAVAGAA
                                                                                                                                                                                                                                                          HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ----SPRGGAVPRKPVS
                                                                                                                                                                                                                                                                                                           -DGPQGRPGYDGYK--GPSGDYGMDGDPGPAPDI-----------
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                                                                                                    SQGEGRÓGEKGESGRPGI PGFQGETGERGNDGNFGERGEKGNMGESRPGPPGMDGSRGRQ
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7.24.1%; Pred. No. u.
7.1ve 24; Mismatches 1
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RESULT 36
Q91AU4
ID Q91AU
AC Q91AU
AC Q91AU
DT 01-Q0
DT 01-Q1
DE Alpha
OS Gall
OC Bukar
OSIAU4;

QSIAU4;

POI-CTI-2000 (TrEMBLrel. 15, Created of the control of the cont
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Best Local Sim
Matches 72;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, BC013581; AAH13581.1; -.

R InterPro; IPR001073; C1q.

R InterPro; IPR001087; Collagen.

R Pfam; PF00386; C1q; 1.

R Pfam; PF01391; Collagen; 7.

R ProDom; PD000007; Collagen; 2.

R PCOSITE; PS01113; C1Q; UNKNOWN 1.

Collagen; Hypothetical protein.

Q SEQUENCE 744 AA; 73364 MW; 2BC1B0955DE2C9A3 CRC64;
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Q96D07;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAGAGGAMCWRRRRAKPSESRHPG------
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                                                                                                                                                                                                                                                                                                                                                                                                               44SQ4---
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                                                                                                                                                                                                                                                                                                                                                                                                             334
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Pred. No. 0.008
16; Mismatches
                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                     Created)
                                         Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PPGEPGLPGIPGPMGPPGAIGFPGPKGEG
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                                         Q25582
ID Q2558
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STRAIN-REED WHITE LEGHORN;

K MEDLINE-20068042; PubMed=10601735;

K MEDLINE-20068042; PubMed=10601735;

K MEDLINE-20068042; PubMed=10601735;

K MEDLINE-20068042; PubMed=10601735;

K Marchant J.K., Foley J.W., Igoe F., Gibney

Nah H.D., Barenbaum M., Myers J.C., Rodriguez E., Dublet

Van der Rest M., Linsenmayer T.F., Upholt W.B., Birk D.E

"Complete primary structure of the chicken alpha1(V) col

"Tomplete primary structure primary structure of the chicken alpha1(V) col

"Tomplete primary structure of the chicken alpha1(V) col

"Tomplete primary structure of the
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ProDom; PD002078; Fib collagen_C; 1
SWART; SW0038; COLF; 1.
SMART; SW0038; LamG; 1.
SWART; SW00282; LamG; 1.
SWART; SW00210; TSPN; 1.
PROSITE; PS00294; PRENYLATION; UNKN
Collagen.
Collagen.
SEQUENCE 1835 AA; 184234 MW; D0
                                                                                                                                                                                                                                    Q25582
Q25582;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                                                                                   Eukaryota; Metazoa; 1
Trichostrongyloidea;
NCBI_TaxID=45464;
                                                                                                                                                                                          Cuticular collagen. COLOST-1.
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NCBI_TaxID=9031;
                                              SEQUENCE FROM N.A.
                                                                                                                                                                Teladorsagia circumcincta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSLGL-GGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GRRGR-----AGSDGARGMPGQTGPKGDRGFDGLAGLPG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEYSPNLWGHEFRSHHDYYIIATSDGTR------EGLESLQGGVCLTRGMKV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGPMGPPG-----SGGLKGEVGEMGPQGPRGIQGPPGP-----AGKP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMGPREAEPGELGIALRGG-----GAADPPFCPHYEKVSGDYGHPVYIVQDGPP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 776
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                  Nematoda; Chro; Haemonchidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184234 MW; D05B9D71022D44B2 CRC64;
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25.7%; Pred. No.
                                                                                                                                                                                                                                       22,2
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                                                                                                                  Chromadorea; Rhabditida;
idae; Ostertagiinae; Telao
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                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                       update)
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Best Local S
Matches 61
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Mol. Biochem. Parasitol. 103:171-181(1999).
EMBL; X96731; CAA65506.1,
InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col cuticle N.
Fiam. PF01391; Collagen; 3.
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SEQUENCE
                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                       InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col cuticle_N.
Pfam; PF01391; Collagen; 3.
Pfam; PF01484; Col_cuticle_N; 1.
                                                                        Mol. Biochem. Parasitol. 80:103-112(1996) EMBL; X96732; CAA65507.1; -.
                                                                                                          MEDLINE=97039674; PubMed=8885226; Johnstone I.L., Shafi Y., Mjaeed A. "Cuticular collagen genes from the
                                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Strongylida,
Trichostrongyloidea, Haemonchidae, Ostertagiinae, Teladorsagia.
NCBI_TaxID=45464,
                                                                                                                                                                                                                                                                                Q25581;
01-NOV-1996
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SEQUENCE
                                                                                                  circumcincta."
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Teladorsagia circumcincta.
                                                                                                                                                                                                                                          Cuticular collagen.
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                                                                                                                                                                                                                                                                                                                                                                        198 APGTLTQGPGSQGPPGPP----GPQGPP---GPDGQPGGPGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŚGNIWREVTRTQ----VLAAP--TRKARQŚ-GĠĠĊĊ------GCĠVŚPAĠPPGP--- 102
                                                                                                                                                                                                                                                                                                                                                                                                                            GG-----RGQPGSPGS-----DGQPGNAGNPGGPGPIGPPGPPGNAGQPG---NAGSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PGQDGQPGSDGRPGQPGRNGPDGPPATPAPDVRPCFNCPPGPPGPAGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
284
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                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
ΑΑ,
                    Col_cuticle_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27534 MW; 60775B7D2CC40C77 CRC64;
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27.2%;
27560 MW;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 141; DB
Pred. No. 0.000
15; Mismatches
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                                                                                                                                                                                                                                                                                                          PRT;
7B76EB6D2DD41D76 CRC64;
                                                                                                                         Α.,
                                                                                                          1., Barry J.
parasitic
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RESULT 39
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Best Local S
Matches 61
                                                                                                                                                                                        Matches
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Best Local :
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 31.3 kDa protein.
T15B7.3.
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                                                                                                                                                                                                                                                                                                                        InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col_cuticle_N.
Pfam; PF01391; Collagen; 3.
Pfam; PF01484; Col_cuticle_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; AF022995; AAB69999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pauley A., Gattung S "The sequence of C. (Submitted (SEP-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                  Hypothetical protein
SEQUENCE 319 AA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                       VGALLLLGVLGLVSGLSL-----EPVYWNSANKRFQAEGG----YVLYPQIGDRLDLLC
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                                                                                            MSASTLVTVASAASGIAIVVCVFTVGMIFNDINSFYDEKIGELKEFKGYEQIA--WQAMI
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PTTRPSSGSS
                                           PRARPPGPHSSPNYEFYKLYLVG------GAQGRRCEA-PPAPNLLLTCDRPDLDL 111
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                                                                                                                                                                                   l Similarity
90; Conserv
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                                                                                                                                                                                     Conservative
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7) to the
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                                                                                                                                                                                   7.6%; Score 141; DE 25.6%; Pred. No. 0.00 tive 27; Mismatches
FLLGRNKRQAECNCGEQSRGCPAGPPGPP----
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EMBL/GenBank/DDBJ
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Pred. No. 0.
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                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                               "Partial characterization of cDNA clones en pro alpha chains of type I collagen from ra Fisheries Sci. 64.780-786 (1998).

EMBL; AB008373; BAA33380.1; -.
Interpro; IPR000097; Collagen.
Interpro; IPR000085; Fib collagen_C.
pfam; PF01410; COLFI; 1.
pfam; PF01410; COLFI; 1.
pfam; PF01391; Collagen; 9.
ProDom; PD000007; Collagen; 1.
ProDom; PD00007; Collagen; 1.
ProDom; PD000078; Fib collagen_C; 1.
SMART; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha 1 type I collagen (Fragment).
Oncorifynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii; Teleostei, Euteleostei, Reprotacanthopterygii; Salmoniformes, Salmonidae, Oncorhynchus.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito
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                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8022;
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 258
                          293
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                         LGIALRGG--GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                               HSLEPGKENLPGDPTSNAT------SRGAEGPLPPPSMPAVAGAAGGLALLL
                                                                                                                                                        ADGAGGKDGVRGMTGPIGPNGPAGSPGDK-----GETGAPGAVGPSGARGAPGERGESGA
                                                                                                                                                                                ATSDGTREGLESLOG-----GVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGA
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 TGPAGRPGELGAAGPP---
                                                                            LGVAGAGGAMCWRRRRAKPSESRHPG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            M., Kunisaki N.,
                                                                                                                                                                                                             61;
                                                                                                                                                                                                                       Similarity
                                                                                                     PGPAGFAGPPGGDGQPGAKGEAGDNGAKGDGGAQGPAGPTGAPGPQGPAGN-----
                                                                                                                                                                                                                                                               809
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                                                                                                                                                                                                                                                              78164 MW;
                                                   -AGPPGATGFPGAAGRFGPPGPSGNNGPPGTPGPGGKEGQKGNRGE
                                                                                                                                                                                                                   7.6%;
27.4%;
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                                                                                                                                                                                                            15;
 -GPKGEKGOPGGDGPNGPSGTP
                                                                                                                                                                                                         Score 141; DB
Pred. No. 0.011
15; Mismatches
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                                                                                                                                                                                                                                                               68C056A7640FCA81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aoki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - PGPSGQPGHSGNDGVPGTPGN
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                                                                            PGSFGRGGSLGLGGGGGGGPREAEPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishida M.,
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                                                                                                                                                                                                            93;
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RESULT 41

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POR PRESENTATION OF PRESENTATI
                                                                                    RRRRR OCCOGGETT
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Q90YC5
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piam; Pr01410; COLPI; 1.—
Piam; Pr01410; COLPI; 1.—
Piam; Pr01391; Collagen; 18.
Piam; Pr00093; VWG; 1
Pr0Dom; PD000007; Collagen; 2.
Pr0Dom; PD002078; Fib collagen_C; 1.
Pr0SITE; PS01208; VWFC; UNKNOWN 1.
PR0SITE; PS01208; VWFC; UNKNOWN 1.
SEQUENCE 1449 AA; 137117 MW; 62E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q910C0
Q910C0;
(TrE)
01-DEC-2001 (TrE)
01-DEC-2001 (TrE)
01-JUN-2002 (TrE)
Collagen al(I)
COLLAL:
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21412237; PubMed=11520665;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
"Identification of ephrin-A3 and novel genes specific to the
"Identification of ephrin-A3 and novel differential display."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q90YC5
Q90YC5;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdner: Oncorhynchus mykisso (Rainbow trout) (Salmo gairdner: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei Actinopterygii; Neopterygii; Teleostei; Salmonidae; Oncorprogramhopterygii; Salmoniformes; Salmonidae; Oncorprogramhopterygii; Salmonidae; Oncorp
                                                                                                                                                                                                                                                                  Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN-A3.
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Saito M., Takenouchi Y., Kunisaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGPAGRPGELGAAGPP-----GPKGEKGQPGGDGPNGPSGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGIALRGG--GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLGLGGGGGMGPREAEPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSLEPGKENLPGDPTSNAT------SRGAEGPLPPPSMPAVAGAAGGLALLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADGAGGKDGVRGMTGPIGPNGPAGSPGDK-----GETGAPGAVGPSGARGAPGERGESGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATSDGTREGLESLQG-----GVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAKGARGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB052835; BAB55661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGPAGFAGPPGGDGQPGAKGEAGDNGAKGDGGAQGPAGPTGAPGPQGPAGN-----
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IPR000885; Fib_colla
IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 19,
(TrEMBLrel. 19,
(TrEMBLrel. 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AGPPGATGFPGAAGRFGPPGPSGNNGPPGTPGPGGKEGQKGNRGE
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Last
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 141; DB
Pred. No. 0.022
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                         (Zebra danio).
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RESULT
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 Query Match
Best Local S
Matches 69
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Best Local
                                                               Waterston R,
"Direct Submission.";
"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; U80444; AAB37788.1;
InterPro; IPR002486; Collagen.
InterPro; IPR002486; Col cuticle_N.
Pfam; PF01391; Collagen; 2.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col cuticle_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; UNKNOWN 1.
SEQUENCE 219 AA; 25146 MW; 7191927E03F8EA01
                                                Hypothetical SEQUENCE 3
                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                Submitted (JAN-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mech. Dev. 107:83-96(2001).
EMBL; AB051678; BAB55891.1;
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  STRAIN=BRISTOL N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P91274
                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a pinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                            Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                CBI_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHWNSSNILLRKE-GYTLQVNVNDYLDIYCPHY----NSSQRGIABQYVLYMVSYRGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN--YEFYKLYLVGGAQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDD-----YDNPEVPKLEKSISGSSPSRDRLLLTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -THIHGRSCLRLRVYVCCSTASDSDDEPQPTEP-----
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 ch 7.6%; S
l Similarity 25.8%; P
69; Conservative 22;
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                                                305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     (Trembirel. 03, Created)
(Trembirel. 03, Last sequence update)
(Trembirel. 19, Last annotation update)
1 30.8 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                             Peloderinae;
                                                                                                                                                                                                                                                                                                                    PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                            Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                              30770 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.6%; Score 140.5;
26.9%; Pred. No. 0.0
cive 27; Mismatcher
Score 140.5; DB Pred. No. 0.004; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. v.v.
7; Mismatches
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                                                6BDC3ADD3E90A358
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                      DB 5;
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                                                CRC64;
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                       Length
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  Indels
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68
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  Gaps
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                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
Pfam;
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z82268; CAB05195.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Matthews L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F52B11.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XUE9
                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the
                                                                                                                                                                                         178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 LRVGQSPRGGAVPRKPVSEMPMERDRGA-----AHSL----EPGKENLPG------
                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
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    LGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSG
                                                                                            AVAGAAG--GLALLLLGVAGAGGAMCWRRRAKPSESRHP-----
                                                                                                                                           CEPITPPPCKPCPQGPAGAPGAPGPQGDAGAPGAP-GQGSGAGAPGPAGPKGASGAPGNP
                                                                                                                                                                                         RKPVSEMPM----ERDRGAAHSLEP-GKENLPGDPTSNATSRGAEGPLPP-----PSMP
                                                                                                                                                                                                                                     EGVDQGSEGAQGGSCSGCCLPGAAGPAGTPG-----KPGRPGRPGAAGLPGNPGRPPAQP
                                                                                                                                                                                                                                                                               DGTREGLESLOGGVCL-----TRGMKVLLRVGQSPRGGAV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPGLAGAPGDSGAP-----GPQGPP 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLRHDPGRCAQCPAGPMGPPGPRGPPGVPGTTGAPG----LDGTPGRHGTPGY---
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                                                                                                                                                                                                                                                                                                                                                                                                              Pro; IPR000087; Coliagen.
Pro; IPR002486; Col cuticle_N.
PP01391; Coliagen; 2.
PP01484; Col cuticle_N; 1.
NCE 304 AA; 29144 MW; 68C73E2551E72DBA CRC64;
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GSFGRGGSLGLGGGGGM------GPREAEPGELGIALRGGGAADPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                   7.6%;
26.8%;
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19,
                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                           Score 140; DB
Pred. No. 0.00
L6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans:
                                                QAGPQGPPGPAGSPGAPGGPGQPGAPGQKG
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       316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          platform
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PSGAPGQPGADGNPGAPGQPGQAGGAGEKGICPKYCAIDG

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RESULT 46
Q9YIB4
ID Q9YIE
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Best Local S
Matches 96
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InterPro; IPR000885; Fib collagen_C.
InterPro; IPR001087; WPF_C.
Pfam; PF01410; CCLFI; 1.
Pfam; PF01391; Collagen; 17.
ProDom; PD000007; Collagen; 1.
ProDom; PD002078; Fib collagen_C; 1.
SMART; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   097405;
097405;
01-MAY-1999
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Collagen pro alpha-chain precursor.
HDCOL 1 ALPHA.
Haliotis discus (Abalone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
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Eur. J. Biochem. 261:714-721(1999).
EMBL; AB017600; BAA75668.1; -.
     Q9YIB4
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MEDLINE=99234051; PubMed=10215888;
Yoneda C., Hirayama Y., Nakaya M., Matsubara Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The occurrence of two types of collagen Walintis discus muscle.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=36094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPPHSGPGGVR---VGALLLLGVLGLVSGLSLEPVYWN--SANKRFQAEGGYVLYPQIGDR 57
                                                                                                                                                                               KVSGDYGHPVYIVQDGPP 330
                                                                                                                                                                                                                                                                                                                                  GPPGSPGAQGP-----PGPSGAT-----GLSGDGGE---RGETGPPGRSGEPGAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTR---EGLESLQGGVCLTRGMKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PGRPGEAGAPGSPGQPGPSG------LVSAKGDRGEAGPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDLLCPRARP------PGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDR 106
                                                                                                                               GLRGDNGNDGAPGQAGPP
                                                                                                                                                                                                                                  MPGLDGAQGERGSPGLNGPSGPPGPVGPQGERGANGFPGSQGEA----GAAGPPGSAGEP
                                                                                                                                                                                                                                                                               ----PGSFGRGGSLGLGGGGG----MGPR-----BAEPGELGIALRGGGAADPPFCPHYE
                                                                                                                                                                                                                                                                                                                                                                               SNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG---
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l Similarity 25.4%;
96; Conservative 2
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1378 AA;
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     PRELIMINARY;
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132583 MW; 6EEE34A65B52E634 CRC64;
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Pred. No. 0.024;
1; Mismatches 125; Indels 13
     PRT;
     1450
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InterPro; IPR000885; Fib collagen_C.
InterPro; IPR000885; Fib collagen_C.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; COLFI; 1.
ProDom; PF01391; Collagen; 18.
ProDom; PF0020007; Collagen; 1.
ProDom; PF0020078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM000314; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen.
SEQUENCE
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alpha 1 type I collagen.
Cynops pyrinogaster (Japanese common newt).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynop
MCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asahina K., Obara M., Yoshizato K.;
"Expression of genes of type I and type II collagen i and development of the blastema of regenerating newt Dev. Dyn. 216:59-71(1999).
EMBL; AB015438; BAA36973.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01208; VWFC; UNKNOWN 1.
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844 APGPKGTRGAAGPPGATGFPGAAGRLGPPGPSGNAGPPGPP
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                                                                                                                                                                                                                                                                                                                                                        GPRGSPGSPGNDGAKGEAGAAGAPGGRGPPGLQGMPGERGSAGMPGAKGDRGDA-----G
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                                                         RGG-----GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                                                                                                                                         TKGADGAPGKDG-ARGLTGPIGPPGPSGAPGDKGEGGPS----GPAGPTGA----
                                                                                                                                                                                                                                                                                            KENLPGDPTSNATSRGAEGPLPPPSMPAVAG--AAGGLALLLLGVAGAGGAMCWRRRRAK 257
                                                                                                                                                                                                                                                                                                                                                                                                                     VPR----KPVSE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GVAGPPGATGAPGKDG----EAGAQG-----PPGPS-GPSGERGEQGPAGSPGFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
103; Conserv
                                                                                                                  PGERGEPGAPGPAGI CGPPGADGQPGAKGESGDAGPKGDAGAPGPAGPTGA-PGPAGNVG
                                                                                                                                                                               PSESRHPG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1450 AA; 137564 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%; Score 139.5; DB ilarity 25.7%; Pred. No. 0.028; Conservative 24; Mismatches 1
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M Yoshizato K.
                                                                                                                                                                         -----PGSFGRGGSLG----LGGGGGMGPREAEPGELGIAL
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   884
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Q9UMG6 PRELIMINARY;
Q9UMG6;
Q9UMG6;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 21, I
01-UN-2002 (TrEMBLrel. 21, I
Collagen type IV a6 chain.
COL4A6.

Created)
Last sequence update)
Last annotation updat

update)

1082

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1024

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Query Match
Best Local S
Matches 61
                                                                                                                                   InterPro; IPRO00087; Collagen.
InterPro; IPRO01442; ProcollagnC4
Pfam; PP01413; C4; 2.
Pfam; PF01391; Collagen; 23.
ProDom; PD000007; Collagen; 4.
ProDom; PD003923; ProcollagnC4; 1
SMART; SM00111; C4; 2.
Collagen.
1690 AA; 163696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL U46961 | HMBL U46961 | HMBL U46961 | HMBL U46967 | HMBL U46967 | HMBL U46971 | HMBL U46981 | HMBL U46991 | HMBL U46999 | HM
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[2]
SEQUENCE FROM N.A.
Zhang X.;
Submitted (JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE OF 1-1644 FROM N.A.

MEDLINE=9629942; PubMed=8661006;

Zhang X., Zhou J., Reeders S.T., Tryggvason K.;

Chang X., Zhou J., Reeders S.T. Collagen COL4A6 gene, which is mut in Alport syndrome-associated leiomyomatosis.";

Genomics 33:473-479(1996).
                                                                                                                                                                                                                                                                                                          mitted (JAN-1996) to the EMBL/Ge UJAN-1996) to the EMBL/Ge UJAN-1004 AAB19039 1; JOINED UJA 6961 AAB19039 1; JOINED UJA 6962 AAB19039 1; JOINED UJA 6962 AAB19039 1; JOINED UJA 6962 AAB19039 1; JOINED UJA 6966 AAB19039 1; JOINED UJA 6966 AAB19039 1; JOINED UJA 6967 AAB19039 1; JOINED UJA 6971 AAB19039 1; JOINED UJA 6972 AAB19039 1; JOINE
       61;
                                    Similarity
          Conservative
                                           25
7
                                                                                                                                              163696 MW;
                                    2,5
          25;
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   Score 139.5;
Pred. No. 0.03
25; Mismatches
                                                                                                                                              4698AE2CC2D3E859
                                    ; DB 4;
          83;
                                                                     Length
          Indels
                                                                                                                                              CRC64;
                                                                     1690;
73;
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MEDILINE=96299642; PubMede8661006;
Zhang X., Zhou J., Reeders S.T., Tryggvason K.;
"Structure of the human type IV collagen CCL4A6
in Alport syndrome-associated leiomyomatosis.";
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047004; AAB19038.1; 046962; AAB19038.1; 046962; AAB19038.1; 046962; AAB19038.1; 046963; AAB19038.1; 046966; AAB19038.1; 046966; AAB19038.1; 046967; AAB19038.1; 046977; AAB19038.1; 046979; AAB19038.1; 046979; AAB19038.1; 046979; AAB19038.1; 046979; AAB19038.1; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 046982; 04
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InterPro; IPR001442; ProcollagnC4
Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen; 23.
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SEQUENCE 1691 AA; 10
                    Jikuya H., Takar
"The nucleotide
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TISSUE=SPLEEN;
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Mammalia; Eutheria; Primates;
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U46990, AAB19038.1;
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 (JAN-2002)
                                Takano J.,
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                                                     N.A.
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                                                                                                                                  (Fragment)
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                    Nomura N., Kikuno
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EMBL/GenBank/DDBJ databases
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                                                                                      Craniata; Vertebrata; I Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         769AA53DD1C7CA87 CRC64;
                                                                                                                                                                                          705
                     R., Nagase T., clone isolated
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                                                                                                   Euteleostomi;
                      Ohara
| from |
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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata X., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata X., Konno H., Adachi J., Pukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Arakawa T., Jara A., Pukunishi Y., Bondo H., Kasukawa T., Saito R.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda T., Mikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shabata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Haysahizaki Y.;
RA Haysahizaki Y.;
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PRINTS; PROGOO7; COMPLEMNTCIQ.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
SEQUENCE 744 AA; 73581 MW;
                                                            InterPro; IPR001073; C1q.
InterPro; IPR001073; Collagen.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; T.
Pfam; PF01391; Collagen; 7.
PRINTS; PR00007; COMPLEMNTC1Q.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Q9D2V4;
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COL8A1.
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01-JUN-2001 (TEMMBLrel. 17, Last sequence up
01-JUN-2001 (TEMMBLrel. 17, Last annotation
procollagen, type VIII, alpha 1.
                                                                                                                                                                                                         Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                       "Functional annotation of a full-length Nature 409:685-690 (2001)
                                                                                                                                                                                                                                                Hayashizaki Y.;
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Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
            C659BDCCBCD6EB9C CRC64;
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ch con	445	296	389	253	334	211	274	169	235	115	199	67	Query Match Best Local Matches 8
Search completed: February 11, 2003, 12:05:05	GEVGPPGMRGLPGPIGPKGEGGHKGLPGLPGVPGLLGPKGEP-G1PGDQGLQGPPGI 500	ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNI 336	PPGEPGLPGIPGPMGPPGAIGFPGPXGEGGVVGPQGPPGPKGEPGLQGPPGKPGFL 444	RRRAKPSESRHPG-PGSFGRGGSLGLGGGGGMGPREAEPGELGI 295	KGEQGLPGLPGPPGLPGVGKPGFPGPKGDRGIGGVPGVLGPRGEKGPIGAPGMGG 388	ATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWR 252	KPGVTGFPGPQGPLGKPGPPGBPQGLIGVPGVQGPPGMAGVGKPGQDGIPGQPGFPGG 333	QSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSN 210	PGLQGPKGEKGFGMPGLPGLKGPPGMHGPPGPVGLPGVG 273	IKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVG 168	PPGPHGLPG IGKPGGPGLPGQPGAKGERGPKGPPGP 234	PPGPHSSPNYEFYKLYLVGGAQGRR-CEAPPAPNLLLICDRPDLDLRFT 114	Query Match Best Local Similarity 23.2%; Pred. No. 0.014; Matches 83; Conservative 28; Mismatches 104; Indels 142; Gaps 18;

Search completed: February 11, 2003, 12:05:05 Job time: 36.2327 secs

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Gapop 10.0 ,
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CA14 MOUSE
CA16 F RIPUS
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p52801 mus musculu
043921 homo sapien
p52802 gallus gall
p52804 gallus gall
p52798 homo sapien
p79728 brachydanio
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O73612
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8 bos taurus
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5 rattus norv
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9 homo sapien
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brachydanio
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P17140 caenorhabdi	P13942 homo sapien	P28481 mus musculu	Q61245 mus musculu	P16252 haemonchus	Q03692 homo sapien	Q00780 mus musculu	P14282 oryctolagus	P02461 homo sapien	P27393 ascaris suu	Q02788 mus musculu	P27658 homo sapien	P05997 homo sapien	P08125 gallus gall	P20849 homo sapien	P32017 gallus gall	P39060 homo sapien

ALIGNMENTS

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FAMILY. FAMILY. Is produced in the produced	Oncogene 13:1343-1352(1996). -i- FUNCTION: MAY PLAY A PIVOTAL ROLE IN FOREBRAIN FUNCTION. BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY). -i- SUBCELLULAR LOCATION: Type I membrane proceini- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN; EXPRESSED IN EMBRYONIC FLOOR PLAYE. ROOF PLAYE AND HINDERAIN SECVENTS.	SEQUENCE FROM N.A. TISSUE=Brain cortex; MEDLINE=96404527; PubMed=8808709; MEDLINE=96404527; PubMed=8808709; Gale N.W., Flenniken A., Compton D.C., Jenkins N.A., Copeland N.G., Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.; "Elk-L3, a novel transmembrane ligand for the Eph family of receptor tyrosine kinases, expressed in embryonic floor plate, roof plate and hindbrain segments";	SEQUENCE PROM N.A. SEQUENCE PROM N.A. SEQUENCE PROM N.A. TISSUE=Brain; MEDLINE=97271551; PubMed=9126477; MEDLINE=97271551; PubMed=9126477; Tang X.X., Pleasure D.E., Ikegaki N.; Tang X.X., Pleasure D.E., Ike	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9608; [1] _ SEQUENCE FROM N.A. Cerretti D.P.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.	RESULT 1 ID = FRB3 HUWAN STANDARD; PRT; 340 AA. ID = SFB3 HUWAN STANDARD; PRT; 340 AA. ID = G15768; 000680; 092875; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DE Ephrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8) DE (LERK-8) (EPH-related receptor transmembrane ligand ELK-L3). DE (LERK-8) GR EPLG8 OR LERKS.

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C 035393
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ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                           Ephrin-B3 precursor. EFNB3.
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035393;
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EMBL; U66406; AAC51203.1; -.
EMBL; U62775; AAC50707.1; -.
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         Bergemann
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Pfam; PF00812; Ephrin; 1.
         MEDLINE=98143367; PubMed=9484836; Bergemann A.D., Zhang L., Chiang
                                     SEQUENCE FROM
                                                                                 Mus musculus (Mouse)
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EXTRACELULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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Pred. No. 3
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EDFF2A23C2FDE79F CRC64;
                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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          M. -K.,
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"Complementary expression of transmembrane ephrins and their receptors and the mouse spinal cord: a possible role in constraining the reference of longitudinally projecting axons.";

To rientation of longitudinally projecting axons.";

L Development 127:1397-1410(2000).

C -!- FUNCTION: MAY PLAY A PIVOTAL ROLE IN FOREBRAIN FUNCTION. BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN CUTTRO. MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF LONGITUDINALLY PROJECTING AXONS.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF025288; AAC53537.1; -. MGD; MGI:109196; Efnb3. InterPro; IPR001799; Ephrin.
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Pred. No. 1.2e
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PDZ RECOGNITION MOTIF (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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Imondi R. Wideman C., Kaprielian Z.;
Imondi R. Wideman C., Kaprielian Z.;
In the mouse spinal cord; a possible role in constraining the
orientation of longitudinally projecting axons.";

Liperelopment 127:1397-1410(2000)

- PUNCTION: MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF
C. LONGITUDINALLY PROJECTING AXONS.

- SUBGUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB4.

- SUBGLIPTIALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
THE FLOOR PLAYE. EXPRESSED ON LATERAL FLOOR PLAYE CELLS,
SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
THE FLOOR PLAYE. EXPRESSED IN CELLS OF THE RETUNAL GANGLION CELL
LAYER DURLING RETUNAL AXON GUIDANCE TO THE OPTIC DISC.

- PENELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE
DERROOD OF COMMISSURAL AXON PATHFINDING.

- PERROD OF COMMISSURAL AXON PATHFINDING.

- SENTILARITY: BELONGS TO THE EPHRIN FAMILY.
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P52800;
P52800;
P52800;
D1-OCT-1996 (Rel. 34, Last sequence update)
D1-OCT-1996 (Rel. 34, Last sequence update)
D1-OCT-1996 (Rel. 41, Last annotation update)
Ephrin-B2 precursor (EPH-related receptor tyrosine (LERK-5) (HTK ligand) (HTK-L) (ELF-2).
EFNB2 OR EPLG5 OR LERK5 OR HTKL OR ELF2 OR EPL5.
                    This SWI
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Cerretti D.P., Vanden Bos T., Nelson N., Kozlosk
Maraskovsky E., Park L.S., Lyman S.D., Copeland
Gilbert D.J., Jenkins N.A., Fletcher R.A.;
"Isolation of LERK-5: a ligand of the eph-relate
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95199254; PubMed=7534404;
Bennett B.D., Zeigler F.C., Gu Q.,
Gillett N., Matthews W.;
"Molecular cloning of a ligand for
tyrosine kinase Htk.";
Proc. Natl. Acad. Sci. U.S.A. 92:18
                                                                                                                                                                                                                                                                                                                                         Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G., "BLF-2, a new member of the Eph ligand family, is segmentally expressed in mouse embryos in the region of the hindbrain and newless."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFB2
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ICR; TISSUE=Brain; MEDLINE=95379837; PubMed=7651410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CB57BL/6J X SJL/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                 MEDLINE=20171264; PubMed=10704386;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (Mouse).
                                 SWISS-PROT
                                                                                                                                                                                                                                                                                                                     Cell. Biol, 15:4921-4929(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
                                                                                                                                                                                                                                                                                                                                  somites."
       ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32:1197-1205(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  92:1866-1870(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fendly B., Goddard A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eph-related receptor tyrosine
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Opeland N.
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and te are r
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; Murinae; Mus
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           SEQUENCE
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Query Match
Best Local
                                                                             P98172;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
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CARBOHYD
CARBOHYD
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SIGNAL
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                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U16819; AAA99708.1; -.
EMBL; L38847; AAC42052.1; -.
EMBL; U30244; AAA82934.1; -.
                                                                        Ephrin-B1 precursor (EPH-re
(LERK-2) (ELK ligand) (ELK
EFNB1 OR EPLG2 OR LERK2 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U30244; AAA622934
MGD; MGI:105097; Efnb2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
NCBI_TaxID=9606;
                        Mammalia; Eutheria;
                                        Eukaryota; Metazoa;
                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GALLLIGVIGLYSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                                                                                                                                                                                                                          WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                      YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 336
                                                                                                                                                                                                                                                                                                                        YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                             GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
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17; EPHRIN.
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336
396
                        Primates;
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                                        Chordata;
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                                                                           EFL-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 637.5;
Pred. No. 1.1
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
PDZ RECOGNITION MOTIF (
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                                        Craniata; Vertebrata; Euteleostomi;
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FROM N.A.

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Query Match
Best Local Sin
Matches 145;
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Davis S., Gale N.W.,
Pawson T., Goldfarb M
Submitted (NOV-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=94349923; PubMed=8070404;
Beckmann M.P., Cerretti D.P., Baum P., Vandenbos T., Ja
Beckmann M.P., Cersetti D.P., Baum P., Vandenbos T., Ja
Farrah T., Kozlosky C., Hollingsworth T., Shilling H.,
Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
"Molecular characterization of a family of ligands for
tyrosine kinase receptors.";
EMBO J. 13:3757-3762(1994).
                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
DOMAIN
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                     Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING TO RIENTARION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY)

-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U09304; AAA53093.1; -.

EMBL; L37361; AAA5309.1; -.

EMBL; U09303; AAB41127.1; -.

EMBL; H136092; CAB86409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fletcher F.A., Huebner Kozlosky C., Druck T., Cerretti D.P., Belmont Submitted (JAN-1997) to
                                                                                                                                                                                                                                                                                                                     PRINTS; PR01347; EPHRIN.
PRODOM; PD0002533; EPHRIN; 1.
PROSITE; PS01229; EPHRIN; 1.
Developmental protein; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (se or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001799; Ephrin.
4
                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: INDUCIBLE PHOSPHORYLATION OF TYROSIN CYTOPLASMIC DOMAIN (BY SIMILARITY). SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDS GRIP1 AND GRIP2.
SUBCELLULAR LOCATION: Type I membrane
TISSUE SPECIFICITY: HEART, PLACENTA, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: BY TNF-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIDNEY, PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                        300035
PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                      PGGVRVGALLLLGVLGLVSGL-----
                                                                                                                                                                                                                                                                                                                                                                                                PF00812; Ephrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC: 3226;
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                   Phosphorylation.
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                                                                                                                                                Conservative
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4;
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'., Simoneaux D.K., Fairweather N.
nt J.W., Beckmann M.P., Lyman S.D.,
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aldrich T.H., Maisonpierre
M., Yancopoulos G.D.;
to the EMBL/GenBank/DDBJ da
                                                                                          34.2%;
                                                                                                                                                    ₹
                                                                                                                                            POTENTIAL.

EXPRACELULIAR (POTENTIAL).

EXTRACELLULIAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).

N-LINKED (GLCMAC. . .) (POTENTIAL).

M, 473DDZFLA5BF89DE CRC64;
                                                                        48;
                                                                        Score 632; DB
Pred. No. 2.5e
18; Mismatches
                                  SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUNG, LIV
                                                                                          DB 1;
.5e-34;
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SEQUENCE FROM N.A.

MEDLINE=98192220; PubMed=9533549;

MCDLINE=98192220; PubMed=9533549;

Wogt T., Stolz W., Welsh J., Jung B., Kerbel R.,

Landthaler M., McClelland M.;

Landthaler M., McClelland M.;

"Overexpression of Lerk-5/Eplg5 messenger RNA:

"Overexpression of Lerk-5/Eplg5 messenger RNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephtin-B2 precursor (Ept-related receptor t)
(LERK-5) (HTK ligand) (HTK-L).
EFNB2 OR EPLGS OR LERKS OR HTKL.
melanomas.";

Clin. Cancer Res. 4:791-797(1998).

Clin. Cancer Res. 4:791-797(1998).

I CONSTRAINING THE OF INCOMPTION THE OF INCOMPTION THE PROJECTING AXONS (BY SIMILARITY).

LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY).

SUBURILLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: LUNG AND KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                        Bennett B.D., Zeigler F.C., Gillett N., Matthews W.;
                                                                                                                                                                                                                                                                                                                                            MEDLINE=96145238, PubMed=8559144;
Cerretti D.P., Vanden Bos T., Nelson N
Maraskovsky E., Park L.S., Lyman S.D.,
Jenkins N.A., Fletcher R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFB2_HUMAN
P52799;
                                                                                                                                                                                 "Molecular cloning of a ligand for tyrosine kinase Htk."; Proc. Natl. Acad. Sci. U.S.A. 92:18
                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=95199254;
                                                                                                                                                                                                                                                                                                                  "Isolation of kinases.";
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TISSUE=Brain;
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Catarrhini; Hominidae
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., Copeland N.
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Matches 135
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_EFB1_CHICK
073612;
15-JUL-1999
15-JUL-1999
16-OCT-2001
        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
EPNB1.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal
SIGNAL
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-i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neuro
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PRINTS; PR01347; EPHRIN.
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                                                                                                                                                                                                                                          DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
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 gallus (Chicken).
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Pred. No. 3.5
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PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
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-i- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB2.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN CYTOPLASMIC DOMAIN (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U72394; AAC07986.1; -.
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MEDLINE=97223524; PubMed=9070326;
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                                                                                                                                                                                                                                                                                                                                                                                               66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 PGGVR---VGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA
GS-----
                                                                                                                                                                                                                  MER-----DRGAAHSL----EPGKENLPGDPTSNA--TSRGAEGPLPPPSMPAVAGA
                                                                                                                                                                                                                                                                                                                                                   EPSKP----YDYYKLYLVKKDQADACSTVMDPNVLVTCNRPEQEIRFTIKFQEFSPNYM
                                       GSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS
                                                                                    SKEADNTVKIVTQSPRHKVPTVEEPGK---PGSVNQNGQETQGPSDGFL--SSKVAVFAA
                                                                                                                                                                                                                                                                 GLEFKRQQDYFITSTSNGTLDGLENREGGVCQTRSMKIVMKVGQDP-NAVIPEQLTTSRP
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-BPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS
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POTENTIAL.

CYTOPLASMIC (POTENTIAL)

PDZ RECCGNITION MOTIF (POT

N-LINKED (GLCNAC. . .) (PO
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Pred. No. 4.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (88 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota; Metazoa; Chordata; Craniata; Ver
Actinopterygii; Neopterygii; Teleostei; Ost
Cyprinidae; Danio.
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ZFIN; ZDB-GENE-990415-67; efnb2a.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
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Durbin L., Brennan C., Shiomi K., Cooke J.,
Shanmugalingam S., Guthrie B., Lindberg R.,
"Eph signaling is required for segmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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PROSITE; PS01299; EPHRIN; 1.
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15-JUL-1999 (Rel. 38, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
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                                                                   DYYIISTSNGTMEGLDNQEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPPKHPDLGG
                                                                                                             DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA
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36724 MW;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PDZ RECOGNITION MOTIF (POTENTIAL).
189ED82372C71C8B CRC64;
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                                                                                                                                                                                                                                                                                                                                                   Score 626.5; DB 1;
Pred. No. 5.4e-34;
4; Mismatches 106;
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WEDLINE=20171264; PubMed=10704386;

I imondi R., Wideman C., Kaprielian Z.;

I complementary expression of transmembrane ephrins and their recept(
in the mouse spinal cord: a possible role in constraining the
in the mouse spinal cord: a possible role in constraining the
crientation of longitudinally projecting axons.";

Development 127:1397-1410(2000).

I prinction: BINDS 70 AND INDUCE THE COLLAPSE OF, COMMISSURAL
AXONS/GROWTH COMES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE
CONSTRAINING THE RECEPTOR TYROSIME KINASES EPHB1 AND EPHA1.

CONSTRAINING THE RECEPTOR TYROSIME KINASES EPHB1 AND EPHA1.

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MEDLINE=95203867; PubMed=7896266;
Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
Jenkins N.A., Gilbert D.J., Copeland N.G., Davison B.L.;
Jenkins N.A., Gilbert D.J., Copeland N.G., Davison of mouse Eplg2
"Genomic organization and chromosomal localization of mouse Eplg2"
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P52795;
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Dev. Biol. 170:420-433 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95014510; PubMed=7929389;
Shao H., Lou L., Pandey A., Pasquale E.B
"CDNA cloning and characterization of a
protein-tyrosine kinase.";
J. Biol. Chem. 269:26606-26609(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-Bl precursor (EPH-related receptor tyrosine
(LERK-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEKS
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01-OCT-1996 (Rel.
30-MAY-2000 (Rel.
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or the Cek5 receptor
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; Murinae; Mus
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receptor ligand)
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kinase ligand

Euteleostomi;
; Murinae; Rattus.

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RESULT 9
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Best Local Sin
Matches 138;
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EMBL; U07599; AACS3247.1; JOINED.
EMBL; U07599; AACS3247.1; JOINED.
EMBL; U07600; AACS3247.1; JOINED.
EMBL; U07600; AACS3247.1; JOINED.
EMBL; U12983; AAAS32311; JOINED.
EMBL; U12983; AAAS32311; JOINED.
MGD; MGI:102708; Efnbl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Pfam, Pf00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \mathtt{PTM}\colon INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES CYTOPLASMIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
                                                                                                                                                                       GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPYYIVQDGPPQSPPNIYYK 339
                                                                                                                                                                                                     VALFAAVGAGCVIFLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALSLSTLASP
                                                                                                                                                                                                                                  LLLLGVAGAGGA---
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                                                                                                                                                                                                                                                                                                                      HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188
                                                                                                                                                                                                                                                                                                                                                                              ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHQEIRFTIKPQEFSPNYMGLEFKKY 129
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               STANDARD;
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37859 MW;
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CYTOPLASMIC (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).
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S -> T (IN REF. 2).
; 8C96FD3DC5CBC405 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 613.5;
Pred. No. 3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
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Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,
Gimpel S., Hollingsworth T., Vandenbos T., Davison B.L.,
Lyman S.D., Beckmann M.P.;
"LERK-2, a binding protein for the receptor-tyrosine kinase ELK, is
evolutionarily conserved and expressed in a developmentally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-Bl precursor (EPH-related receptor tyrosine (LERK-2) (ELK ligand) (ELK-L).
EFNBl OR EFIG2 OR LERKO.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                               SEQUENCE
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Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                          Developmental protein; Neurogenesis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01347; EPHRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING TO RIENTATION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY) SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB3 (PREFERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC DOMAIN (BY SIMILARITY). SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHB1 AND EPHB2.
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: INDUCIBLE PHOSPEORYLATION OF TYROSINE RESIDUES
                                                                                                       AHSLEPGKENLPGDPTSNATSRGAEGP---
                                                       HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA
                                                                                                                                             AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--
                              HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT
                                                                                    ---YEYYKLYLVRPEQAAACSTVLDPŃVLVŤCNKPQQEIRFTIKFQEFSPNYMGLEFKKY
                                                                                                                                                                                                     al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation.
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Rodentia;
                                                                                                                                                                                                                    38.0%;
                                                                                                                                                                                                                                                               37951 MW;
                                                                                                                                                                                                     52;
                                                                                                                                                                                                                 Score 608.5;
Pred. No. 8.2
                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
PDZ RECGNITION MOTIF (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL)
; 183045C5C7358F7E CRC64;
                                                                                                                                                                                                                                                                                                       SPHRIN-B1.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Sciurognathi; Muridae;
                                                                                                                                                                                                      Mismatches
   --LPPPSMPAVAGAAGG--
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8.2e-33;
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Indels Length

65;

Gaps

10;

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236 188 192 129

345;

(POTENTIAL)

Glycoprotein;

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O13097;
01-NOV-1997
01-NOV-1997
              CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                             Signal;
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burppean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=97316777; PubMed=9174051;

Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.;

"Identification of Klerk, an Eph family ligand regulated during mesoderm induction and neurogenesis in Xenopus laevis.";

Oncogene 14:2159-2166(1997).

-!- FUNCTION: MAY HAVE A ROLE IN THE DEVELOPING MESENCHYMAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
Ephrin-Bl precursor (EPH-related receptor tyrosine (LERK-2) (ELK ligand) (ELK-L) (XLERK).
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                                                       TRANSMEM
DOMAIN
DOMAIN
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Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
                                                                                                                                                   ProDom, PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neuroo
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ++
                                                                                                                                                                                               Pfam; PF00812; Ephrin; 1
PRINTS; PR01347; EPHRIN
                                                                                                                                                                                                                          EMBL; U31427; AAC35995.1; -. InterPro; IPR001799; Ephrin.
                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189
                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: IN THE ADULT, EXPRESSED AT LOW LEVELS IN ADULT TISSUES WITH INCREASED LEVELS OBSERVED IN THE KIDNEY, OCCYTES, OVARY AND TESTIE.
PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE CYTOPLASMIC DOMAIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NERVOUS TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALSLSTLASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345
                                                                                                                                         mental protein; Neurogenesis; Transmembrane; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSK
                             327
225
246
327
327
131
131
                 ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a; Craniata; Ver
Mesobatrachia;
                            N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
PDZ RECOGNITION MOTIF (
                                                                                                 EPHRIN-B1.
EXTRACELLULAR
                71230CE7F6BE5974 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pipoidea; Pipidae;
                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase ligand
                                                          (POTENTIAL)
                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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RESULT 11
EFA2_BRARE
ID EFA2_B
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Best Local Sim
Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                        EFA2_BRARE STANDARD; PRT; 195 AA.
179727;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine
(LERK-6) (ELF-1) (ZFEPHL3).
EFNA2 OR EFLG6 OR LERK6.
                                      -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDERAIN OF DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT I EXPRESSED THROUGHOUT THE MIDERAIN INCLUDING THE REGION OF THE PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADIFASHION THROUGHOUT THE TECTUM.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                               be involved in the creation o
zebrafish.";
Development 124:655-664(1997)
                                                                                                                                                                                                                                                  MEDLINE=97195707; PubMed=9043080;
Brennan C., Monschau B., Lindberg R.,
Bonhoeffer F., Holder N.;
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; 'Cyprinidae; Danio.
This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                     -!- FUNCTION: CONTROL AXON OF THE RETINO-TECTAL M-!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                           Eph receptor tyrosine kinase ligands control nvolved in the creation of the retinotectal ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLEFRRNQDYXITSTSNSTLQGLENREGGVCQTRSMXIIMKVGQDP--NAVPPEQLT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QP-----YEYYKLYMVRRDQLEACSTVIDENVLVTCNQPGKEYRFTIKFQEESPNYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIRRLIGHLIVLYRLCSALGKNIEPVTWNSQNPRFISGKGLVLYPEIGDRIDIICPKGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVR--VGALLLLGVLGLVSGLSLEPVYWNSANKRPQAEGGYVLYPQIGDRLDLLCPRA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSKIAVFAAIGAGCVIFILIIIFLVVLLIKIRKRHRKHTQQAAALSLSTLASPKCSGNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLLGVAGAGGAMC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MERDRGAAHSLEPGKENLPGDPTSNATSRGA-EGPLPPP-----SMPAVAGAAGGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TTRPSKE----ADNTGKIATFGPWNGPVONPGKSDTNLSDKPTGRWGVDGFF
                                                                                                                                                                                                                                                                                                                                                                                               rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                               (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.4%;
                                                                                                                                                       MAP.
: Attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----WRRRAKPSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                  GROWTH
                                                                                                                                                                                                                                                                                                                                                                  (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 600; DB 1;
Pred. No. 2.8e-32;
3; Mismatches 100
                                                                                                                                                                                  AND MAY BE INVOLVED
                                                                                                                                                       to the membrane
                                                                                                                                                                                                                                                                    Guthrie B.,
                                                                                                                                                                                                                           map
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                                                                                                                                                                                                                           axon
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                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase
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                                                                                                                                                        b
                                                                                                                                                                                     IN THE CREATION
                                                                                                                                                                                                                                                                                                                                                                     Cypriniformes;
                                                                                                                                                                                                                           growth
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327;
                                                                                                                                                          GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand
     a collaboration -
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                                                                         GRADED
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outstation

THYMUS,

PROSTATE,

TESTIS,

OVARY,

SMALL INTESTINE,

AND PERIPHERAL

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Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                   P52797;
01-OCT-1996
01-OCT-1996
15-JUL-1999
Ephrin-A3 pr
           MEDLINE=95063919; PubMed=7973638; Davis S., Gale N.W., Aldrich T.H., Maisonpierre Pawson T., Goldfarb M., Yancopoulos G.D.; "Ligands for EPH-related receptor tyrosine kinas membrane attachment or clustering for activity." Science 266:816-819(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia: Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement (See httor send an email to license@isb-sib.ch).
                                                                                                                                       Cerretti D.P., Beckmann M.P.;
"Ligands for the receptor tyrosine kinases
cDNAs encoding a family of proteins.";
Oncogene 10:299-306(1995).
                                                                                                                                                                                             MEDLINE=95140419; PubMed=7838529;
Kozlosky C.J., Maraskovsky E., Mc
Teepe M., Lyman S.D., Srinivasan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZFIN; ZDB-GENE-990415-66; efna2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y09668; CAA70863.1; -
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          EFNA3 OR EPLG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210
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 SUBCELLULAR
TISSUE SPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
                                                                                                                                                                                                                                                                                                                                                                                                                           MAMDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSQRCGADGPC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLK-----LKVYV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EHRMRGFKRWECNRPQSPDGPLRFSEKFQLFTPFSLGFEFRPGHEYYYISSPHPNHAGKP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAPPAPNLLLTCDR----PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYWNSSNSRFW-QGEYTVAVSINDYLDVYCPYYESPQPHS--RMERYILFMVNHDGYLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                      996 (Rel. 34, Created)
996 (Rel. 34, Last sequence update)
999 (Rel. 38, Last annotation update)
99 (Rel. 38, Last annotation update)
9 precursor (EPH-related receptor tyrosine kinase ligand
(EHKI ligand) (EHK1-L).
 SPECIFICITY: EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Neurogenesis; Glycoprotein;
1 1 POTENTIAL.
17 195 EPHRIN-A2.
32 N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                          OR LERK3
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22688 MW;
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S
                                                                                                                                                                                           / E., McGrew
nivasan S., F
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                                                                                                                                                                                                                                                                                                                          EFL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 185; DB
Pred. No. 1.2e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9EE284FEB61D0C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KPTSS--
 H
 IN BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                           "J.T., Vandenbos T.,
Fletcher F.A., Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                           238
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..2e-05;
71;
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 membrane by
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                                                                                 P.C.,
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                                                       that require
                                                                                                                                                                   elk: isolation
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                                                                                                                                                                                                                                                                                               Euteleostomi;
 y a GPI-a
MUSCLE,
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                                                                                 Lhotak V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195;
 GPI-anchor.
SCLE, SPLEEN
                                                                                                                                                                                              R.B.
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CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                P52801;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyr
(LERK-6) (ELF-1) (CEK7-1igand) (CEK7-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-s
Cheng H.U., Flanagan J.G.;
"Identification and cloning of ELF-1,
ligand for the Mek and Sek receptor t
Cell 79:157-168 (1994).
                                 STRAIN-Swiss Webster; TISSUE-Brain; MEDLINE-95007776; PubMed-7522971; Cheng H.J., Flanagan J.G.;
                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                       EFA2 MOUSE
                                                                                                                                                                                                                                  HOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U14187; AAC50078.1; -. EMBL; L37360; AAA52368.1; -.
                                                                     SEQUENCE FROM N.A.
                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 601381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                175
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44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOOD LEUKOCYTES.
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                         GPG-----
                                                                                                                                                                                                                                                                                                      RKPVSEMP----
                                                                                                                                                                                                                                                                                EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
                                                                                                                                                                                                                                                                                                                                                   QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP
                                                                                                                                                                                                                                                                                                                                                                          SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF
                                                                                                                                                                                                                                                                                                                            QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
                                                                                                                                                                                                                                                                                                                                                                                                ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL----DLRFTIKF
                                                                                                                                       OR EPLG6 OR LERK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:3223; EFNA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AA;
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23
38
67
100
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                                                                                                                             (Mouse)
                                                                                                                                                                                                                         STANDARD;
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238
38
67
100
                                                                                                      Chordata;
Rodentia;
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
MISSING (IN REF. 2).
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 179;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPHRIN-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                      Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                       PRT;
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                                                                                                                                        OR EPL6.
             , a developmentally tyrosine kinases.";
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thi; Muridae;
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
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MBL outstation -
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A2 HUMAN

EFA2 HUMAN

J 0439Z1, 076020;

T 15-DEC-1998 (Rel. 37, Created)

T 15-DT-1999 (Rel. 38, Last sequence update)

JT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ephrin-A2 precursor (EPH-related receptor tyros:

/*T.FRK-6) (HEK7-11gand) (HEK7-L).
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EFA2_HUMAN
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Best Local S
Matches 58
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Interpro; IPR001799; Ephrin.
Interpro; IPR001799; Ephrin; 1.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U14941; AAA53636.1; -.
EMBL; U14752; AAA68520.1; -.
EMBL; MGI:102707; Efna2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., "CDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the I (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine J. Biol. Chem. 270:3467-3470(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95181289; PubMed=7876076;
                                                                                                                                                                                                                                                                              152
                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lycoprotein;
IGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                  VYWNSANKRFQAE----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA
                                                                                                                                                                                                                          EAPEPIFTSNSSCSGLGG
                                                                                                                                                                                                                                                   GDP----TSNATSRGAEG
                                                                                                                                                                                                                                                                                                       REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPWSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                   GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISATP--
                                                                                                                                                                                                                                                                                                                                                            QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT
                                                                                                                                                                                                                                                                                                                                                                                         VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                               58
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                              -PNLVDRPCLR--LKVYVR
                 ; Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
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170
184
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EPHRIN-A2.

N-LINKED (GLCNAC..

N-LINKED (GLCNAC..

N-LINKED (GLCNAC...

F1997545F25B9ABC C
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 176;
Pred. No. 4.
                 Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . ) (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; L
1.9e-05;
1es 69;
                                                                                 tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 209;
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                                                                                   kinase
                              Euteleostomi;
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                                                                                                          Query Match
Best Local &
Matches 43
                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            EMBL; U92896; AAC39577.1; -...
EMBL; U92893; AAC39577.1; JOINED.
EMBL; U92894; AAC39577.1; JOINED.
EMBL; AC004258; AAC04896.1; -..
EMBL; AJ007292; CAA07435.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.;
"Cloning, chromosal mapping, and tissue expression of the gene
"Cloning the human Eph-family kinase ligand ephrin-A2.";
Biochem. Biophys. Res. Commun. 252:378-382(1998).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise
Trankheim M., Amico-Keller G., Coeiield J., Duarte S., Lucas S.,
Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerretti D.P., Nelson N.; "Characterization of the genes for mouse LERK-3/Ephrin-A3 mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 conservation of intron/exon structure."; Genomics 47:131-135(1998).
                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                           Pfam; PF00812; Ephrin; 1
PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                    Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99045414; PubMed=9826538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                ProDom; PD002533;
PROSITE; PS01299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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[1]
                                                                                                                                                                                                                                                                                                        nterPro;
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39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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                                                                                                                                                                                                                                                                                                                      602756;
                         VYWNSANKRFQA-----BGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYBFYKLYLVGGA
VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PABRMEHYVLYMVNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                   l Similarity
43; Conserv
                                                                                                                                                                                                                                                                                                                                 HGNC:3222; EFNA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                       IPR001799; Ephrin.
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25
42
174
188
6
25
29
213
                                                   Conservative
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                                                                                                                                                                                                                                    GPI-anchor;
                                                                                                          Α,
                                                                                                                                                                                                                                                  EPHRIN;
                                                                                                          23878 MW;
                                                               36.88;
                                                                                                                                                                                                                                 1.
1.
Signal.
                                                     14;
                                                                                                                    BPHRIN-A2.

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

R -> A (IN REF. 3).

AA -> RR (IN REF. 3).
                                                                  Score 175.5;
Pred. No. 5.
                                                                                                                                                                                                                       POTENTIAL.
                                                                                                          33C9FB1A8168B2D0
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                             .4e-05;
51;
                                                                                 BB
                                                                                                           CRC64;
                                                                               Length
                                                      Indels
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                                                                                                                                                                (POTENTIAL)
(POTENTIAL)
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                                                                                 213;
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                                                     Gaps
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QGRRCEAPPAPNILLICDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS

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EFA2_CHICK
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                                                                                                                                                                            Query Match
Best Local S
Matches 49
                                                                                                                                                                                                                                      CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                      InterPro; France, Printin; 1.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand (LERK-6) (ELF-1).
                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95360981; PubMed=7634327; Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.; Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.; "Complementary gradients in expression and binding of ELF-1 and Mek4 in development of the topographic retinotectal projection map."; Cell 82:371-381(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE TECTUM BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L40932; AAC42229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHA5 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFNA2 OR EPIG6 OR LERK6 OR ELF1
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                                                                                                                   7
   FSLGFEFRPGHEYYYISAS
                              NLWGHEFRSHHDYYIIATS 141
                                                        EEPLP--AERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLKFSEKFQLFTP
                                                                                     RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
                                                                                                                     AALLAAI VG-
                                                                                                                                            ALLILGVIGIVSGISLEP-----VYWNSANKRFQAEGGYVLYPQIGDRIDLLCPRA
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161
175
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1 22
23 200
36 36
161 161
175 175
                                                                                                                   -VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVEVSINDYLDIYCPHY 64
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N-LINKED (GLCNAC. ...) (POTI N-LINKED (GLCNAC. ...) (POTI N-LINKED (GLCNAC. ...) (POTI N-LINKED (GLCNAC. ...) (POTI N-LINKED (GLCNAC. ...) (POTI N-LINKED (GLCNAC. ...)
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                                                                                                                                                                          Score 172; DB 1;
Pred. No. 8.5e-05;
6; Mismatches 58
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                                                                                                                                                                                                     Length 200;
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) (POTENTIAL)
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RESULT 16
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Best Local S
Matches 73
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SEQUENCE
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SIGNAL
CHAIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update
30-NAY-2000 (Rel. 39, Last annotation upda
Ephrin-A5 precursor (EPH-related receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: INDUCES GROWTH CONE COLLAPS:
GANGLION CELL AXONS.
-1- SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE 95360980; PubMed 7634326;
Drescher U., Kremoser C., Handwerker C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFNA5 OR RAGS. [Follows]
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X90377; CAA62027.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 82:359-370(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "In vitro guidance of retinal ganglion tectal protein related to ligands for E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonhoeffer F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Posterior tectum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00812; Ephrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
160
                                           170
                                                                                                                                           113
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                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                  16 LLLLGVLGL-VSGLSLEP------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR
                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
-PANSCMKTIGVHDRVFDVNDKVENŠLEPADDTV---RESAEPSRG-ENAAQTPRIPIRL
                                           SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A
                                                                                          FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS-----CLK--LKVFVR---
                                                                                                                                     FTIKFQEYSPNLWGHEFRSHHDYYIIATS---DGTREGLESLQGGVCLTRGMKVLLRVGQ 169
                                                                                                                                                                                                                                                                                      MILLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQ-QGDYHIDVCINDYLDVFCPH
                                                                                                                                                                                                                                     ARPPGPHSSPNYEFYKLYLVG------GAQGRRÇEAPPAPNLLLTCDRPDLDLR 112
                                                                                                                                                                                         YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPN-----GPLK
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                                                                                                                                                                                                                                                                                                                                                                                   73;
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37
228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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37
26206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenesis; Glycoprotein; GPI-anchor; Signal POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                   Score 170.5; DB 1
Pred. No. 0.00012;
0; Mismatches 91
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N-LINKED (GLCNAC. . .) (F
% 56D8E4FBDECF18AD CRC64;
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Eph receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                     91;
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                                                                                                                                                                             Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentiies requires a license agreement (See http://www.isb-sib.ch/andentiies requires and the EMBL outset (See http://www.isb-sib.ch/andentiies requires andentiies requires and the EMBL outset (See http://www.isb-sib.ch/andentiies requires and the EMBL outset (See http://www.isb-sib.ch/andentiies requires and the EMBL outset (See http://www.isb-sib.ch/andentiies and the EMBL outset (See http://www.isb-sib.ch/andentiies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blood 95:221-230(2000).
-!- FUNCTION: WAY PLAY A ROLE IN THE INTERACTION BETWEEN ACTIVATED LYMPHOCYTES AND DENDRITIC CELLS IN TONSILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=95140419; PubMed=7838529;
KOZIOSKY C.J., Maraskovsky E., McGrew J.T.,
Teepe M., Lyman S.D., Srinivasan S., Fletch
Cerretti D.P., Beckmann M.P.;
"Ligands for the receptor tyrosine kinases
cDNAs encoding a family of proteins.";
Oncogene 10:299-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFA4_HUMAN STANDARD; PRT; 201 AA. P52798; O95457; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Ephrin-A4 precursor (EPH-related receptor tyr
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U14188; AAC50079.1; -.
EMBL; AJ006352; CAA06992.1; -.
EMBL; AJ006353; CAA0693.1; -.
                                                                                                                                 Glycoprote:
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFNA4 OR EPLG4 OR LERK4.
                                                                                                                                                                                                                                                                                                                                                                     Genew;
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is secreted by activated human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 2 isoforms; 1/GPI-anchored (shown he 2/secreted; are produced by alternative splicing.
TISSUE SPECIFICITY: EXPRESSED IN THE ADULT SPLEEEN, LYMPH PROSTATE, OVARY, SWALL INTESTINE, AND COLON, AND IN FETAL LUNG, LIVER AND KIDNEY. ALSO DETECTED IN HEMATOPOIETIC CEISINILARITY; BELONGS TO THE EPHRIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                 HGNC:3224; EFNA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
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                                                                                                                                                          GPI-anchor;
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the E., Funderud S.,
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1.
Signal; Alternative
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      POTENTIAL.

EPHRIN-A4.

REMOVED IN MATURE FORM (
N-LINKED (GLCNAC. . .) (
GPI-ANCHOR (POTENTIAL).
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Fletcher
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er F.A., Gayle R.B. III,
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Best Local (
                  This SWISS-PROT entry is copyright. It is produced through a collaborative of the Swiss Institute of Bioinformatics and the EMBL outstate between the Swiss Institute of Bioinformatics and the Embl outstate. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 35,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFA5 BRARE
P79728;
01-NOV-1997
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Development 124:655-664(1997).
EMBL; Y09669;
ZFIN; ZDB-GENI
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Bonhoeffer F., Holder N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97195707; PubMed=9043080; Brennan C., Monschau B., Lindberg
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DEVELOPMENTAL STAGE: EXCRESSED IN THE PRESUMPTIVE MIDERAIN OF
DEVELOPING EMBRYOS FROM THE SIZONITE STAGE: BY 24 HOURS IT IS
STRONGLY EXPRESSED IN THE MIDERAIN CAUDAL TO THE PRESUMPTIVE
TECTUM. AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN
OF THE TECTUM.
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ZDB-GENE-980526-186;

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Best Local S
Matches 72
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EFA1
                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    (IERK-1) (XBLF).

(EFNAI OR EPGLI OR ELF.

Xenopus laevis (African clawed frog).

Xenopus, Metazoa, Chordata, Craniata, Vertebrata, E

Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea,

Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                    MEDLINE=97000306; PubMed=8843391; Weinstein D.C., Rahman S.M., Ruiz J.C., Hemm "Embryonic expression of eph signalling fact Mech. Dev. 57:133-144(1996).

1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Developmental
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Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                  similarity).
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                             SIMILARITY).
SUBCELLULAR LOCATION: Attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIKFQEYSPNLWGHEFRSHHDYYIIA---TSDGTREGLESLQGGVCLTRGMKVLLRVGQS
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U31204;
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37
228 AA;
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AAA74485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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37
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N-LINKED (GLCNAC. . .) (P
74B3406C05418E6E CRC64;
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Pred. No. 0.0
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LOW AFFINITY TO
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; Pipidae;
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о врна1
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Matches
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Best Local (
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_HUMAN
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CARBOHYD
VARSPLIC
                                              MEDLINE=97392664; PubMed=9245480;
Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K.;
"LERK-7: a ligand of the Eph-related kinases is developmentally
regulated in the brain.";
Cytokine 9:540-549(1997).
                                                                                                                                            Winslow J.W., Moran P., Valverde J., Shih A., Tsai S.P., Goddard A., Henzel W.J., Hefti F.; "Cloning of AL-1, a ligand for an Eph-related receptor involved in axon bundle formation.", Neuron 14:973-981(1995).
                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                               EFA5
MEDLINE=20069483; PubMed=10601038;
Davy A., Gale N.W., Murray E.W., Klinghoffer
                                                                                                                                 Neuron
[2]
                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                           EFNA5 OR EPLG7 OR LERK7.
                                                                                                                                                                                                                                                                                                                                                                P52803;
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ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
Glycoprotein; GPI-anchor;
                           FUNCTION
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Ephrin-A5 precursor (EPH-related receptor tyrosine
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                                                                                                           TISSUE=Brain
                                                                                                                                                                                                       MEDLINE=95267434; PubMed=7748564;
                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Primates;
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Alternative splicing;
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Pred. No. 0.00018;
6; Mismatches 93;
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TPPPUNVHTPRSHIQSDEPEVPLPGVMKSVAGNSAAPGTPC
TLYGLLLAALLIRL -> SE (IN ISOFORM A').
; 1B3A508E0A7B872E CRC64;
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N-LINKED (GLCNAC
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  Soriano
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RESULT 21
EFA5_MOUSE
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Best Local S
Matches 65
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feuerstein C., Robbins S.M.;

(Compartmentalized signaling by GPI-anchored ephrin-A5 requires the "Compartmentalized signaling by GPI-anchored ephrin-A5 requires the "Compartmentalized cellular adhesion.";

Genes Dev. 13:3152-3135(1999).

-!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.

INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAPACIAE-LIKE MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF 1 COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE.
        EFRAS MOUSE STANDARD; PRT; 228 AA 00854; 008544; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Ephrin-A5 precursor (EPH-related receptor t. (LERK-7) (AL-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http:\overline{/}/www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: ATTACHED TO THE ME IS COMPARTMENTALIZED IN DISCRETE CAVEOLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MICRODOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                          VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601535;
                                                                                                                                                                                                                                                                                 S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                                                                                                                                                                                                                                                                                                 DHTSKGFKRWECNRPHSPN------GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                                                                                                                                                                                                                           VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
                                                                                                                                                                                            PADDTV---HESAEPSRG
                                                                                                                                                                                                                          PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA
                                                                                                                                                                                                                                                       AI PDNGRRS
                                                                                                                                                                                                                                                                                                                                             ----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:3225; EFNAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
37
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
37
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.1%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26297 MW;
                                         (EPH-related receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurogenesis;
                                                                                                                                                                                                                                                       CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE
                                                                                                                                                                                            -ENAAQTPRIPSRL----LAILLFLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : ATTACHED TO THE MEMBRANE IN DISCRETE CAVEOLAE-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

EPHRIN-A5.

N-LINKED (GLCNAC. . .) (PORTE (PORTE )

N -> K (IN DBSNP:469062).

/FTId=VAR_012035.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 167.5;
Pred. No. 0.00
Ps Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6893B1CCACFF3F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPI-anchor; Signal;
                                           kinase
                                                                                                                                                                                            223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPHA2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228;
                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
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RESULT 22
EFA5_RAT
ID EFA5_RAT
AC P97605;
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STANDARD;

PRT;

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Matches
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Best Local
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SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND EPHB1 (BY SIMILARITY).

SUBCELULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARIMENTALIZED IN DISCRETE CAVEOLAB-LIKE MEMBRANE MICRODOMAINS (BY SIMILARITY).

ALTERNATIVE PRODUCTES: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "HUBLINE=97060319; PubMed=8903354; Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.; "Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis."; Dev. Biol. 179:382-401(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U90664;
EMBL; U90665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental
  187
                                           198
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                                                                                       142
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rPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                          VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
                                                                                                                                                                                                                                                                                                                      VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG-----
                                                                                                                                   S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                         PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA
                                                                                                                                                                                  DHTSKGFKRWECNRPHSPN--
                                                                                                                                                                                                                              ----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
PADDTV---HESAEPSRG-ENAAQTPRIPSRL----LAILLFLLA
                                                                                          AI PDNGRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00812; Ephrin;
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            splicing
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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AAB50240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; Neurogenesis; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                        9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                          -CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₩;
                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                  Score 167.5;
Pred. No. 0.00
29; Mismatches
                                                                                                                                                                                  ----GPLKFSEKFOLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

EPHRIN-A5.

N-LINKED (GLCNAC. . .) (PO
MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              85439F5337420022
                                                                                                                                                                                                                                                                                                                                                                                            .00019;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                      Indels
       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                     228;
                                                                                                                                                                                                                                                                                                                                                                      51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                        197
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Query Match
Best Local S
Matches 65
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15-DEC-1998 (Rel. 37,
30-MAY-2000 (Rel. 39,
Ephrin-A5 precursor (
(LERK-7) (AL-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley;

Li Y.Y., McTiernan C.F., Feldman A.M.;

"rLERK7, rat ligand for Eph-related receptor tyrosine kinase.";

"submitted (MAR-1998) to the EWEL/GenBank/DDBJ databases.

-i- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON PASCICULATION.

-INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE

MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOWAIN OF ITS

MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOWAIN OF ITS
                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Winslow J.W., Moran P., Valverde J., Shih A., Tsai S.P., Goddard A., Henzel W.J., Heffi F., "Cloning of AL-1, a ligand for an Eph-related receptor involved in axon bundle formation.", Neuron 14:973-981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL S
STRAIN=Sprague-Dawley;
MEDLINE=95267434; PubMed=7748564;
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EFNAS OR EPLG7 OR LERK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U69279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winslow J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )evelopmental
142
                                               141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE (BY SIMILARITY).
SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: EXPRESSED IN BRAIN, H
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BPHB1 (BY SIMILARITY).
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE MICRODOMAINS (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, FLACENTA AND LUITISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART,
AIPDNGRRS-----CLK--LKVFVR----PTNSCMKTIGVRDRVFDVNDKVENSLE
                                               S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                                                                                  DHTSKGFKRWECNRPHSPN-----GPLKFSEKFOLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                                                 VYWNSSNPRFQ
                                                                                                                                                                                                                                                 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYBFYKLYLVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00812; Ephrin;
                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                n 9.1%;
Similarity 28.8%;
55; Conservative 2
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                                                                                                                                                 GAQGRRCEAPPAPALLITCDRPDLDLRFTIKFQEYSPALWGHEFRSHHDYYIIAT
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37
228
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(Rel. 37, Last sequence update)
(Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
1 20 POTENTIAL.
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A
                                                                                                                                                                                                    -RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
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37
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                                                                                                                                                                                                                                                                                                                                                                                                        ₩;
                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                   Score 167.5;
Pred. No. 0.00
29; Mismatches
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N-LINKED (GLCNAC. . .) (F
, 855985532D580022 CRC64;
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receptor tyrosine kinase ligand
                                                                                                                                                                                                                                                                                                                           .00019;
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, Beck K.D., Caras
i tyrosine kinase
                                                                                                                                                                                                                                                                                                      81;
                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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Matches
                       Query Match
                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK-1) (Immediate early response protein B61) (Tumor necrosis
factor, alpha-induced protein 4).
EFNA1 OR EPGL1 OR LERKI OR TNFAIP4.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 23
HUMAN
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P20827;
                                                                                                       Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN;
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91042512; PubMed=2233719;
Holzman L.B., Marks R.M., Dixit V.M.;
Holzman L.B., Marks R.M., Dixit V.M.;
Particles and encodes a secreted protein.
Mol. Cell. Biol. 10:5830-5838(1990).
                                                                                CHAIN
                                                                                            Glycoprotein;
SIGNAL
                                                                                                                                                                                                                     EMBL; M57730; AAA58388.1; -. PIR; A36377; A36377.
                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDILINE=95140419; PubMed=7838529; WEDILINE=95140419; PubMed=7838529; WCGrew_J.T.,
                                                                                                                                                                                          MIM; 191164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                             InterPro; IPR001799; Ephrin.
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              Local
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46;
              Similarity
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18
26
205 AA;
Conservative
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                                                   205 E
26 N
23771 MW;
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Primates;
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             9.0%;
27.5%;
31;
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EPHRIN-A1.
N-LINKED (G
Score 166; DB
Pred. No. 0.00
%1; Mismatches
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                                                       CRC64;
                        Length
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 16;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Ephrin-Ai precursor (EPH-related receptor tyrosine kinase ligand 1)
Ephrin-Ai precursor (EPH-related receptor tyrosine kinase ligand 1)
Ephrin-Ai (Immediate early response protein B61).
EFNAI OR EPGLI OR LERKI.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                           CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi H., Ikeda T.;
"Molecular cloning and expression of rat and implications on organogenesis.";
Oncogene 11:879-883(1995).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KEPHAS, EPHAS AND EPHA7. ALSO BINDS WITH I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFA1 RAT P97553;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
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MEDLINE=95405853; PubMed=7675446;
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                                                                                                                                                                                                                                                                     InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                              EMBL; D38056; BAA07242.1;
                                                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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YYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERD-----
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                                 RYSLYMVEHQEYVTCEPQSKDQVRVKCNQPSAKHGPEKLSEKFQRFTPFTLGKEFKEGHS 125
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                                                                                                       LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYE
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                                                         FYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHD 134
                                                                                LLGLCCSLAAVDRHIVFWNSSNPKFREE-DYTVHVOLNDYLDIICPHYEDDSV-ADAAME
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PD002533; Ephrin; 1.
; PS01299; EPHRIN; 1.
otein; GPI-anchor; Signal.
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                                                                                                                                         Similarity
                                                                                                                                                                            205 AA;
                                                                                                                              Conservative
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23718 MW; CB6DAB3DB56A6EAD CRC64;
                                                                                                                                        8.8%;
                                                                                                                             33;
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EPHRIN-A1.
N-LINKED (
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                                                                                                                                        Score 162.5; DB 1;
Pred. No. 0.00036;
                                                                                                                              Mismatches
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CARBOHYD
CONFLICT
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"Molecular cloning and expression implications on organogenesis.";
Oncogene 11:879-883(1995)
                                                                     Glycoprotein;
SIGNAL
                                                                                                                                                             EMBL; D38146; BAA07344.1; -.
EMBL; U26188; AAA67563.1; -.
EMBL; U90662; AAB50237.1; -.
   CONFLICT
                                                                                           Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
                                                                                                                                        MGD; MGI:103236; Efnal.
InterPro; IPR001799; Ephrin.
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   18
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74
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                                                                                   GPI-anchor;
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1.
Signal
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FAI MOUSE

DE CONTINUE (Rel. 34, Created)
FAI OLOCTINGE (Rel. 35, Last sequence update)
FAI OLOCTINGE (Rel. 35, Last annotation update)
FAI OLOCTINGE (REL. 39, Last annotation update)
FAI CONTINUE (REH-FAI TERRELL)
FAI MOUSE
FAI 
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"Distinct and overlapping expression patterns of ligands for
"Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).

-i- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris J.C., Ciarletta A., Morris G.E., Giannotti Hammett D.J., Finnerty H., Turner K., Wood C.R.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ data
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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POTENTIAL.
EPHRIN-A1.
N-LINKED (GLCNAC. .
N-Y (IN REF. 1).
A -> T (IN REF. 1).
Q -> E (IN REF. 1).
N -> K (IN REF. 1).
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01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
 EMBL;
                                                                                                                                                      "Characterization of the genes for mouse LERK-3/Ephrin-A3 mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 conservation of intron/exon structure."; Genomics 47:131-135(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EV
                                                                                                                                                                                                                                               Flenniken A.M., Gale N.W., Yancopoulos G.D., "Distrinct and overlapping expression pattern Eph-related receptor tyrosine kinases during Dev. Biol. 179:382-401(1996).
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                        or send an
                                                                                                                        - 1 - SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                            - !- SUBCELLULAR LOCATION: Attached to the membrane
                                                                                                                                                                                              Cerretti D.P.,
                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=129;
                                                                                                                                                                                                                                                                                       MEDLINE=97060319; PubMed=8903354;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                             EFNA4 OR EPLG4 OR LERK4 OR
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U90663;
U92890;
U92889;
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                                                  requires a license agreement
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                                        email to license@isb-sib.ch).
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AAB50238.1; -.
AAC39962.1; -.
AAC39962.1; JO:
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Rodentia;
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Pred. No. 0
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Sciurognathi;
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Best Local 9
SEQUENCE OF 51-000
STRAIN-DBA/2J;
STRAIN-B=92267014; P
MEDLINE=92267014; P
                                                                                         SEQUENCE FROM N.A.
STRAIN=129/Sv; TISSUB=Liver;
STRAIN=3238750; PubMed=8477738;
KCNGR R.Y.C., Kwan K.M., Lau E.T.,
Grant M.E., Cheah K.S.E.;
                                                                                                                                                                                                                                                                                                             CAIA MOUSE STANDARD; PRT; 6

Q05306;

Q1-NOV-1995 (Rel. 32, Created)

O1-NOV-1995 (Rel. 32, Last sequence up

O1-NOV-1995 (Rel. 32, Last annotation

CO11agen alpha 1(X) chain precursor.
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ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
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Mammalia; Eutheria;
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                                                           "Intron-exon structure, alternative the mouse collagen X gene, Coll0a-1. Eur. J. Biochem. 213:99-111(1993).
                                                                                                                                                                               MEDLINE=93143576; PubMed=8424763;
Elina K., Berola I., Rosati R., Metsa
Elina K., Evenia I., Rosati R., Metsa
de Crombrugghe B., Vuorio E.;
"The mouse collagen X gene: complete
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                                                                                                                                                           Biochem. J.
                                                                                                                                                            structure and expression pattern."; Biochem. J. 289:247-253(1993).
                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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      PubMed=1587271;
M.F., Hayashi M.,
                                       FROM N.A.
                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
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Pred. No. 0.0
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N-LINKED (GLCNAC...) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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EMBL; X65121; CAA46237.1; -.
EMBL; X65121; CAA46231.1; -.
EMBL; Z21610; CAA79736.1; -.
EMBL; Z2807; S2807.
PIR; S21216; S31216.
PIR; S22215; S22215.
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InterPro; IPR001087; Collagen.
Pfam; PF00386; Ciq; 1.
Pfam; PF01391; Collagen; 9.
PRINTS; PR00007; COMPLEMNTC1Q.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: HOMOTRIMER.

-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-!- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92182017; PubMed=1543751;
Elima K., Metsaeranta M., Kallio J.,
Garofalo S., de Crombrugghe B., Vuor
"Specific hybridization probes for m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of the human and mouse type X collagen genes and mapping the mouse type X collagen gene to chromosome 10."; Eur. J. Biochem. 206:217-224(1992).
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Biochim. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular matrix; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:88445; Coll0al.
211
                                                                                                     Local
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FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                          MGPPHSGPGGV-RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PR00007; COMPLEMNTC1Q.
; PD000007; Collagen; 2.
SM00110; C1Q; 1.
                                                                                   Similarity
97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 385-627 FROM N.A
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-ĠPSGVGRRGENGFPGQPGI----
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19 560
19 560
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6 248
8 248
4 417
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56775 MW;
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                                                                                     Conservative
                                                                                                     25.5%;
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                                                                                 30;
                                                                                                                                                                                  NONHELICAL REGION (NC1)
C1Q.
P - L (IN REF. 3).
P - S (IN REF. 2).
L -> F (IN REF. 3).
T -> S (IN REF. 3).
T -> L (IN REF. 3).
T -> L (IN REF. 3).
R -> K (IN REF. 3).
R -> K (IN REF. 3).
I -> H (IN REF. 3).
I -> H (IN REF. 3).
C - T (IN REF. 3).
C - T (IN REF. 3).
                                                                                 Score 159; DB 1; I
Pred. No. 0.002;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                            COLLAGEN ALPHA 1(X) CHAI:
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
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                                                                                                                                                                      -> T (IN REF. 3)
FE984CA99AF708E2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Hydroxylation;
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                                                                                                                         Length
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                                                                                     Indels
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EMBL outstation -
                                                                                   146;
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Lang H., Glanville R.W., Fietzek P.
"The covalent structure of calf skin acid sequence of the cyanogen bromic (positions 552-788).";
Hoppe-Seyler's Z. Physical
                                                                                                                                                                                                                                                                             acid sequence of the (positions 1-222). Hoppe-Seyler's Z. F
                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
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                                                                                                            amino acid sequence of the cyanogen bromide peptide alph (positions 403-551).";
                                                                                                                                                                                                         SEQUENCE OF 243-422.

MEDLINE=80026027; PubMed=488907;

Dewes H., Fietzek P.P., Kuhn K.;

"The covalent structure of calf
acid sequence of the cyanogen br

(positions 223-402).";
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20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updatcollagen alpha 1(III) chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA13
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Bentz H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-242.
MEDLINE=80026026;
Fietzek P.P., Allm
                                                                                                                                                                                                                                                                                                                                    Kuhn
                                                                                                       Hoppe-Seyler's
                                                                                                                                                                           SEQUENCE OF 423-571
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mann H., Rauter
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i bromide
                                zek P.P., Kuhn K.;
lf skin type III collagen.
bromide peptide alpha 1(I)
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              360:841-850(1979).
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le peptide
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the alpha
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Best Local S
Matches 60
P17656;
01-AUG-1990 (Rel.
01-AUG-1990 (Rel.
15-JUN-2002 (Rel.
Cuticle collagen
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InterPro; IPR000087; Collagen.
InterPro; IPR001007; VWF_C.
PR01391; Collagen; 17.
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"The covalent structure of calf skin type III collagen. VI. The amino acid sequence of the carboxyterminal cyanogen bromide peptide alpha 1(III)CB9B (positions 928-1028).";

Hoppe-Seyler's Z. Physiol. Chem. 360:861-868(1979).

-I-FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONNECTIVE TISSUES ALONG WITH TYPE I COLLAGEN.

-I-SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE ALSO CROSS-LINKED VIA HYBROXYLYSINES.

-I-PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=80026030; PubMed=488910;
Dewes H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen. V. The
acid sequence of the cyanogen bromide peptide alpha 1(III)CB9A
(position 789-927).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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Probom; PD000007; Collagen; 1.
PROSITE; PS01208; VWFC; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 948-1049.
MEDLINE=80026031; PubMed=488911;
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                                                                                                                                                                                                            GGAMCWRRRAKP-----SESRHPGP-----GSFGRGGSLGLGGGGGMGPREAEPGE 292
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 (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 41, Last annotation update)
lagen 2 precursor.
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                                                                 STANDARD;
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26.5%;
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HYDROXYLATION.
HYDROXYLATION.
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Pred. No. 0.006;
9; Mismatches
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'; 8EEC33D1C66EC9A3 CRC64;
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InterPro; IPR0002486; Col cutic.
InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col cuticle N;
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                              Signal
SIGNAL
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EMBL; Z68301; CAA92
PIR; B31219; B31219
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=85105075; PubMed=2578467; Kramer J.M., Cox G.N., Hirsh D.; Expression of the Caenorhabditis elegans collagen col-2 is developmentally regulated."; J. Biol. Chem. 260:1945-1951(1985).
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

-i- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kramer J.M., Cox G.N., Hirsh D.;
"Comparisons of the complete sequences Caenorhabditis elegans.";
Cell 30:599-606(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                        Cuticle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coles L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MEDLINE=83050944; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COL-2 OR W01B6.7
                                                                               168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
 189
                           218
                                                       129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CUTICULAR COLLAGEN FAMILY.
 GPAGPAGNDGAPGAPGG----PGEPGASEQGGP-
                           GPLPPPSMPAVAGAAGGLALLLLGVAGA----GGAMCWRRRRAKPSESRHPGP-GSFGRGG
                                                                               GQSPRGGAVPRKPVSEMPMERDRG------AAHSLEPGKENLPGDPT--SNATSRGAE
                                                     GNPGKGASAPCEPVTQPPCQPCPGGPPGPAGPAGPPGPPGPDGNPGSPAGPSGPGPAGPP
                                                                                                                                                                                                                                                                                                                                                                                J01048; AAA27990.1; -. V00148; CAA23464.1; -. Z68301; CAA92620.1; -.
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                        Connective
                                                                                                                                                              1
38
85
105
153
183
215
301 AA;
                                                                                                         Conservative
                                                                                                                                       37
38
301
85
97
134
176
212
282
282
28025 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7139711;
                                                                                                                                                                                                                                                                                        tissue;
                                                                                                                       8.2%;
                                                                                                                                                                                                                                                                                                                                           cuticle_N.
                                                                                                           15
                                                                                                                                                              CUTICLE COLLAGEN 2.
GLY-RICH.
TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                                                                        Repeat; Multigene
                                                                                                                       Score 151.5; DB 1;
Pred. No. 0.0027;
                                                                                                           Mismatches
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  -GEPGPAGPPGPAGPAGNDG
                                                                                                                                                                                                                                                                                      family;
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                                                                                                                                     Length
                                                                                                           Indels
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                                                                                                                                                                                                                                                                                        Collagen;
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                                                                                                                                       301;
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236
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Q01955; Q9BQT2;
01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last seque)
15-JUN-2002 (Rel. 41, Last annot collagen alpha 3 (IV) chain precipility.
                                                                                                                                                                                                         MEDLINE=91353570; PubMed=1882840;
Morrison K.E., Mariyama M., Yang-Feng T.L., Reeders S.
"Sequence and localization of a partial cDNA encoding
3 chain of type IV collagen.";
Am. J. Hum. Genet. 49:545-554(1991).
                                                                                                                                                                                                                                                                                       J. Biol.
[5]
                                                                                                                                                                                                                                                                                               Quinones S., Bernal D., Garcia-Sogo M., Elena S.F., Saus J.; "Exon/intron structure of the human alpha 3(TV) gene encompassing the Goodpasture antigen (alpha 3(TV)MC1). Identification of a potentially antigenic region at the triple helix/NC1 domain junction."; J. Biol. Chem. 267:19780-19784 (1992).
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                    Ding J.;
Submitted (JAN-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                  Heidet L., Arrondel C., Forestier L., Cohen-Solal L., Mollet Gutierrez B., Stavrou C., Gubler M.C., Antignac C., "Structure of the human type IV collagen gene COL4A3 and muta autosomal Alport syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., VARIANTS AS E-297; R-407; Q-1215; S-1277; T-1330; E-1334; E-1347 AND C-1 E-162; Y-236; H-408; R-451; L-574; E-1269 AND MEDLINE=21064696; PubMed=11134255; MEDLINE=21064696; PubMed=11134255;
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                                                                                                                                                                                   SEQUENCE
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Mammalia; Eutheria;
    SEQUENCE
                                                                  SEQUENCE
                                                                                          J. Clin.
                                                                                                                                            Turner N., Mason
                                                                                                                                                                        TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                "Molecular cloning
                                                                                                                                                        MEDLINE=92147878;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
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                                                                                         the alpha
in. Invest.
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S-1277; T-1330;
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                                                                OF 1644-1670
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rol. 12:97-106(2001).
                                                                                                                                           P.J.,
                                                                                         89:592-601(1992).
                                                                                                                                        PubMed=1737849;
                                                                                                     of the human Goodpasture chain of type IV collagen.
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Primates;
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    AND
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    ALTERNATIVE
                          EMBL/GenBank/DDBJ databases
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    SPLICING
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                                                                                                                                            Povey
                                                                                                                   antigen
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-1661, AN
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ng the
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VARIANTS R-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  mutations
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NIDGEN.

NIDGEN.

NIDGEN.

1. SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIBLE HELIX STRUCTURE WITH 2 COTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

1. SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).

1. ALTERNATIVE REDOUCTS: AT LAST 3 ISOFORMS; 1 (SHOWN HERE), 2/V AND 3/L5; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR C-TERMINAL NC1 DOWAINS.

1. COMMAIN (NC1 DOWAINS.

1. COCHLEA, LUNG AND PRESENT ONLY IN BASEMENT MEMBRANES OF KIDNEY, EYE, COCHLEA, LUNG AND BRAIN.

1. DOWALN: ALPHA GOTYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOWAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE GAY.Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELLIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL DOWAIN.

1. POMS: FLEXIBILITY IN THE TRIPLE HELLIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELLIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE OF THE TRIPLE HELIX). AND A SHORT N-TERMINAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE OF THE TRIPLE HELIX). AND A SHORT N-TERMINAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE OF THE TRIPLE HELIX). AND A SHORT N-TERMINAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE OF THE TRIPLE HELIX). AND A SHORT N-TERMINAL TRIPLE-HELIX AND A SHORT N-TERMINAL TRIPLE-HELIX AND ADDITIONAL N-LINKED GLYCOSYLATION SITE.

1. PIM: TYPE IV COLLAGENS CONTAIN NUMBEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF THE SILOCATED IN THE NCI DOWAIN, ARE CONSERVED IN ALL KNOWN TYPE TO COLLAGENS IN THE NCI DOWAIN, ARE CONSERVED IN ALL KNOWN TYPE
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"Mutations in the type IV collagen alpha 3 (COL4A3) gene in autos mutations in the type IV collagen alpha 3 (COL4A3) gene in autos recessive Alport syndrome.";

Hum. Mol. Genet. 3:1269-1273(1994).

-!- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOWERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE' MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Alternative splicing of the NCI domain of the human alpha 3(I collagen gene. Differential expression of mRNA transcripts tha predict three protein variants with distinct carboxyl regions J. Biol. Chem. 269:2342-2348(1994).
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Bernal D., Quinones S., Saus J.;
"The human mRNA encoding the Good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Kidney;
MEDLINE=94124597;
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Lemmink H.H., Mochizuki
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       IV COLLAGENS.

IV COLLAGENS.

PTM: Phosphorylated by the Goodpasture antigen-binding protein.

PIME PROSPHORYLATED BY AGAINST THE NC1 DOMAIN OF ALPHA3(IV) MEDIATE

DISEASE: ANTIBODIES AGAINST THE NC1 DOMAIN OF ALPHA3(IV) MEDIATE

THE HUMAN AUTOIMMUNE DISEASE, GOODPASTURE SYNDROME, WHICH IS

CHARACTERIZED BY HEMATURIA AND PULMONARY HEMORRHAGE.

DISEASE: DEFECTS IN COL4A3 ARE ASSOCIATED WITH THE TYPE I

AUTOSOMAL RECESSIVE FORM OF ALFORT SYNDROME, AN HEREDITARY

GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE REMAL FAILURE,

GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE REMAL FAILURE,

HEMATURIA AND DEAFNESS. THE RECESSIVE FORM OCCURS EQUALLY BETWEE:
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AND DEAFNESS.
FEMALES.
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rimuki T., van den Heuvel L.P.W.J.,
Brunne
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y the Goodpasture antigen
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P39061; Q62002; Q61437;

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Collagen alpha 1(XVIII) chair
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (SHORT AND LONG ISOFORMS).

Rehn M., Hintikka E., Pihlajaniemi T.;

"Characterization of the mouse gene for the alpha-1 chain of type
XVIII collagen (CCL18A1) reveals that the three variant N-terminal
polypeptide forms are transcribed from two widely separated
promoters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (SHORT ISOFORM).

STRAIN=BALB/c; TISSUB-Liver;

MEDLINE=94245707; PubMed=8188673;

Rehn M.V., Hintikka E., Pihlajaniemi T.;

Rehn M.V., Hintikka E., Pihlajaniemi of mouse type XVIII collaguerial structure of the corresponding gene, and comparison of the partial structure of the corresponding the alpha 1 (XVIII) chain with its homologue, the alpha 1 (XV) collagen
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                                                                            Oh S.P., Kamagata Y., In Technology of Gly-Xaa-Yaa repeats
                                                                                                                                                                                                                                 "Alpha 1(XVIII), a collagen chain collagenous sequence, a distinct t with type XV collagen.";
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                                                                            94240111; PubMed=8183893;
Kamagata Y., Muragaki Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97160848; PubMed=9008168;
O'Reilly M.S., Boehm T., Shing Y., Fu
Flynn E., Birkhead J.R., Olsen B.R.,
"Endostatin: an endogenous inhibitor
                                                                                                                SMART; SM00282; LamG; 1.

SMART; SM00210; TSPN; 1.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Glycoprotein; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                              MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM AND A LONG FORM (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

PIM: PROLINES AT THE THIRD POSITION OF THE TRIPBEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
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J. 17:1656-1664 (1998).

J. 17:1656-1664 (1998).

FUNCTION: ENDOSTATIN POTENTLY INHIBITS ENDOTHELIAL CELL

PROLIFERATION AND ANGIOGENESIS. MAY INHIBIT ANGIOGENESIS

PROLIFERATION AND ENDOTEMBER PROTEOGLYCANS INVOLVED IN
                                                                                                                                                                                                                                                                                                            MGI:88451; Col18a1
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                                                                                                                                                                                                                                                IPR000087; Collagen.
IPR001791; Laminin_G.
IPR003129; TSPN.
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; AAA20657.1; -.
; AAC52901.1; -.
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AAA19787.1;
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DDMEGS-GIPLWTTARSSDGLQGPPGSP
                             EKVSGDYGHPVYIVQ----DGPPQSP
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TRIPLE-HELICAL REGION 6
NONHELICAL REGION 6 (NC
TRIPLE-HELICAL REGION 7
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Pred. No. 0.0
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MISSING (IN SHORT ISOFORM).
AVPTOLIPFOSILQAPLGRESAPPDF -- MAPRWHLLDVL
TSLVLLLYARVSWAE (IN SHORT ISOFORM).
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N-LINKED (GLCNAC.
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NONHELICAL REGION 10 (NC10).

TRIPLE-HELICAL REGION 10 (COL10).

NONHELICAL REGION 11 (NC11).
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Gaill F., Wie- TMOLECULAR CAND. J. MOL Biol. -!- FUNCTION: -!- SUBUNIT: -!- SUBUNIT: -!- PTM: ALL PIR; S22915; Interpro; IPR Bornar Glycoproteein; DOWAIN HOD RES MOD	01-JUL-1993 (Rel. 26, Cr. 01-JUL-1993 (Rel. 26, La. 15-JUL-1998 (Rel. 36, La. 18-JUL-1998 (Rel. 36, La. 18-JUL-1998 (Rel. 36, Riftidae, Riftid
Wiedem Charac Charac To: Howc 1917 Collec 1917 Collec 1917 Collec 1013 1024 1034 1034 1034 1034 1034 1034 1034 103	3 (Rel. 3 (Rel. 3 (Rel. 3 (Rel. 9 (Rel.) 10 (Rel.) 11 (Rel.) 12 (Rel.) 13 (Rel.) 14 (Rel.) 15 (Rel.) 16 (Rel.) 16 (Rel.) 17 (Rel.) 18 (Rel.) 19 (Rel.)
Gaill F., Wiedemann H., Mann K., "Molecular Characterization of coffeed and worms collected at deep sea J. Mol. Biol. 221:209-223(1991) FUNCTION: FIBRIL-FORMING COL FUNCTION: FIBRIL-FORMING COL FUNCTION: FIBRIL-FORMING COL FUNCTION: FIRRIL-FORMING COL FUNCTION: FIRRIL-FORMING COL FORM: ALL THE "X" ARE PROBABI. IPRO00097; Collagen; 16 PTM: ALL THE "X" ARE PROBABI. TO 1.2	01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence 15-JUL-1998 (Rel. 36, Last annotati Fibril-forming collagen alpha chain Riftia pachyptila (Tube worm). Eukaryota, Metazoa, Pogonophora, Ve Riftida, Riftidae, Riftia. NCBI_TaxID=6426; [1] SEQUENCE. MEDLINE=93130909; PubMed=1483468; MARIN K., Gaill F., Timpl R., "Amino-acid sequence and cell-adhes collagen from the tube worm Riftia hydrothermal vents."; Eur. J. Biochem. 210:839-847(1992). [2] SEQUENCE OF 8-45; 525-618 AND 810-8 TISSUE-Cuticle;
TOROXYLAN INDROXYLAN I	01-JUL-1993 (Rel. 26, Created) 15-JUL-1993 (Rel. 26, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) Fibril-forming collagen alpha chain. Riftil pachyptila (Tube worm). Riftida, Riftiidae; Pegonophora; Vestimentifera; Axonobranchia; Riftiida; Riftiidae; Riftia. NCBI_TaxID=6426; [1] SEQUENCE. MEDLINE=93130909; PubMed=1483468; MEDLINE=93130909; PubMed=1483468; MANIN K., Gaill F., Timpl R.; "Amino-acid sequence and cell-adhesion activity of a fibril-for collagen from the tube worm Riftia pachyptila living at deep se bydrothermal vents."; Eur. J. Biochem. 210:839-847(1992). [2] SEQUENCE OF 8-45; 525-618 AND 810-882. MEDLINE=92015209. PubMed=1920405:
c., Timpl R., Engel J.; and interstitial collagens chermal vents."; SYLATED HYDROXYLYSINES. SEGION (N-TERMINAL). ICAL REGION (C-TERMINAL). ITON (PARTIAL).	a; Axonobranchia; y of a fibril-forming living at deep sea
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Matches 82
                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Cartilage;
TISSUE=Cartilage;
MEDLINE=91113131; PubMed=1703407;
Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
Thomas J.T., Kwan a.P.L., Grant M.E., Boot-Handford R.P.;
"Isolation of cDNAs encoding the complete sequence of bowine
"Isolation of cDNAs encoding the complete sequence of mammalian type
                                                                                                                                                                                                                                                                                                                                       CA1A BOVIN
P23206;
01-NOV-1991
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VARTANT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel.
01-NOV-1991 (Rel.
15-JUL-1999 (Rel.
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                      Collagen alpha 1(X)
                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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                                                    SUBUNIT: HOMOTRIMER.

PTW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEAUNT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.

SIMILARITY: CONTAINS 1 CLQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPRGMPGTAGSPGQAGAXGDGGPTGEQGRPGAPGVXGSSGPP------GDVGAPGHA 294
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1027 AA;
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Institute. Trutions as long
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Pred. No. 0
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                                            _HUMAN CALIF HUMAN STANDARD; PRT; 1516 AA.

CALH HUMAN STANDARD; PRT; 1516 AA.

P39060; Q9Y6Q8; Q9Y6Q7; Q9UK38;

01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)

COLlagen alpha 1 (XVIII) chain precursor (Contains:

COLLBAL.
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MOD_RES
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Pfam; PF00391; Collagen; 9.
PRINTS; PR000007; COMPLEMNTC1Q.
ProDom; PD000007; Collagen; 1.
SMART; SM00110; ClQ; 1.
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Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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DOMAIN
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Extracellular matrix; Connective
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InterPro; IPR000087; Collagen.
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HYDROXYLATION (BY S.

HYDROXYLATION (BY S.

N-LINKED (GLCNAC. . .

W; CD4CA73A03E004CA (
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NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
C10.
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Pred. No. 0.016;
0; Mismatches 125;
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   Craniata; Vertebrata; Catarrhini; Hominidae;
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(BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GER-GLNGPKGDIGPAGLPGP
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RA IUGhetti P., Suzuki O., Goddi P.H., Alves V.A., Sertie A.L.,
RA Zorick T., Soares F., Camargo A., Moreira E.S., di Loreto C.,
RA Moreira-Filho C.A., Simpson A., Oliva G., Passos-Bueno M.R.;
RT For the development of prostatic adenocarcinoma.";
RI Cancer Res. 61:7375-7378 (2001)
CC -1- FUNCTION: COLAISA PROBASLY PLAYS A MAJOR ROLE IN DETERMINING THE
RETINAL STRUCTURE AS WELL AS IN THE CLOSURE OF THE NEURAL TUBE.
CC -1- FUNCTION: ENDOSTATIN POTENTLY INHEITS ENDOTHELIAL CELL
PROLIFERATION AND ANGIOGENESIS. MAY INHEIT ANGIOGENESIS BY
RACTOR SIGNALLING.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM/NC1-303 AND A LONG
PORM/NC-493 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: PRESENT IN MULTIPLE ORGANS WITH HIGHEST LEVELS
IN LIVER, LUNG AND KIDNEY.
-1- PTM: PROLITES THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
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A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Menzel U., Palabar J., Kumpf K., Kawasaki K., Asakawa S.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A Remser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A Mehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
The DNA sequence of human chromosome 21.";
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MEDLINE=98164096; PubMed=9503365;

Saarela J., Ylikarppa R., Rehn M., Purmonen S., Pihlajaniemi T.;

"Complete primary structure of two variant forms of human type X collagen and tissue-specific differences in the expression of the corresponding transcripts";

Matrix Biol. 16:319-328(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of cDNA and genomic DNA encoding human type XVIII collagen and localization of the alpha I(XVIII) collagen gene to mouse chromosome 10 and human chromosome 21."; Genomics 19:494-499(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sertie A.L., Sossi V., Camargo A.A., Passos-Bueno M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhi-Yong H.,
"Cloning and
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Genet. 9:2051-2058(2000).
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SMART; SM00210; TSPN; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Glycoprotein; Signal; Alternative spli
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EMBL; AF184060; AAF01310.1;
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GlycoSuiteDB; P39060; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:2195; COL18A1.
                                                                                                                                                                         CARBOHYD
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-> T (IN REF. 4).
-> Y (IN REF. 4).
3C70F29A4476EE76 (
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                               Ueyama N., Wu
n S., Li M., Na
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                                 Wu J.
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                               H.D.
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                  DATE DE POSOS RE
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Best Local S
Matches 64
            Homo sapiens (Human).
Eukaryota, Metazoa, C
Mammalia, Eutheria; P
NCBI_TaxID=9606;
[1]
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InterPro: IPR000087; Collagen.
Pfam; PF01391; Collagen; 11.
ProDom; PD000007; Collagen; 1.
Extracellular matrix; Connective ti
Glycoprotein; Cartilage; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                            -CA19 HUMAN STANDARD; PRT; 921 AA. P20849; Q9Y6P2; Q9Y6P3; Q9H151; Q9H152; Q9922 01-FEB-1991 (Rel. 17, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Collagen alpha 1(IX) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
SIGNAL
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                                                                                                               COL9A1
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                                                                                                                                                                                                                                                                                                                              PGPPGPPGMPGFKGHTGHKGGPGBIGKEGEKGSPGPPGPPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGAAGEAGLPGLP----GVDGLTGT-----DGPPGPNGPPGDRGALGPAGPPGPAGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAVAGAAG--GLALLLLGVAGAGGAMCWRRRRAKPSESRHPG------
                                                                                                                                                                                                                                                                                                                                                                     -GAADPPFCPHYEKVSGDYGHPVYIVQDGP----
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675 I
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
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"Cloning and developmental expression of the alpha 3 chain of chi
type IX collagen.";

J. Biol. Chem. 267:10070-10076(1992).

-I-FUNCTION: COLLAGEN TYPE IX IS A MINOR CARTILLAGE NONFIBRILLAR
COLLAGEN. IT IS ASSOCIATED WITH TYPE II COLLAGEN FIBRILS.
-I-SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1ALPHA 2(IX), AND ALPHA 3(IX).

-I-PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATIONIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. TRIPEPTIDE REPEATING ALPHA 1(IX) of chicken

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tissue; Repeat; Hydroxylation;

COLLAGEN ALPHA 3 (IX) CHAIN.
TRIPLE-HELICAL REGION 3 (COL3).
NONHELICAL REGION 2 (COL2).
TRIPLE-HELICAL REGION 2 (COL2).
TRIPLE-HELICAL REGION 1 (COL).
TRIPLE-HELICAL REGION 1 (COL).
TRIPLE-HELICAL REGION 1 (COL).
TRIPLE-HELICAL REGION 1 (COL).
NONHELICAL REGION 1 (NC1).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GICNAC. . .) (POTENTIAL)
N-LINKED (GICNAC. . .) (POTENTIAL)

RVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSM RVG--PQGPPGPRGPPGPSGKDGIDG----EPGPSGLPGPP------1; Length 71; Indels 675; GPKGAPGK 78; Gaps 9 225 12;

PGSFGRG-

115 272

PGPPGPPGPSGLPGGNGFRGPPGPSGLPGFPGPPGPPGLAGIIPEGGGDLQCPALCP -GSLGLGGGGGM----GPR-----EAEPGELGIALRGG------- POSPENI 336 300

Craniata; Vertebrata; Catarrhini; Hominidae; RT; 921 AA. Q9H152; Q99225; Q13699;

Q13700;

Euteleostomi;

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EMBL;
EMBL;
EMBL;
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"Human COL9A1 and COL9A2 genes. Two genes of 90 and 15 kb code for "Human COL9A1 and COL9A2 genes. Two genes of 90 and 15 kb code for similar polypeptides of the same collagen molecule.";
Matrix Biol. 17:237-241(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Nickerson T., Harley
Submitted (DEC-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olsen B
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MEDLINE-89137096; PubMed=2465149;
Kimura T., Mattei M.-G., Stevens J.W., Goldring M.B., Ninomiya Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE=98370844; PubMed=9707347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of rat and human type IX collagen cDNA and localization of the alpha 1(IX) gene on the human chromosome (Eur. J. Biochem. 179:71-78(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
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SUBUNIT:
3(IX) ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lysine-derived cross-links.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING, DOMAIN: EACH SUBULIT IS COMPOSED OF THREE TRIPLE-HELICAL DOMAINS INTERSPERSED WITH NONCOLLAGENOUS DOMAINS. THE GLOBULAR DOMAIN AT THE WITH NONCOLLAGENOUS DOMAINS. THE GLOBULAR DOMAIN AT THE WITH DOMAIN STYPE IX COLLAGEN MOLECULES REPRESENTS THE NC4 DOMAIN WHICH MAY PARTICIPATE IN ELECTROSTATIC INTERACTIONS WITH POLYANIONIC GLYCOSAMINOGLYCANS IN CARTILAGE.

PTM: COVALENTLY linked to the telopeptides of type II collagen by the covalently linked to the telopeptides
                                                                                                                  X54413; CAA38277.1;
AF036110; AAC33527.1;
AF036111; AAC33527.1;
AF036111; AAC33527.1;
AF036111; AAC33527.1;
AF036113; AAC33527.1;
AF036114; AAC33527.1;
AF036115; AAC33527.1;
AF036116; AAC33527.1;
AF036116; AAC33527.1;
AF036117; AAC33527.1;
AF036117; AAC33527.1;
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                                                AF036118;
AF036119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAA38276
                                                                                                                  AAC33527.1;
AAC33527.1;
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7.11 JOINED
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MBL outstation -
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Glycoprotein; Collagen;
SIGNAL 1
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Pfam; PF02210; TSPN; 1.
ProDom; PD000007; Collagen; 1.
SMART; SM00210; TSPN; 1.
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MIM; 120210;
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PIR; S02140; S02140.
PIR; S13580; S13580.
Genew; EGNC:2217; COL9A1.
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SEQUENCE
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InterPro; IPR001791; Laminin_C
InterPro; IPR003129; TSPN.
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M32133; AAA53474.1; JOINED.
M32137; AAA53475.1; -.
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PLEPERETCHELPARITYSQTTDE -> WAWTA LLIGLCLCAAQ (IN SHORT ISOFORM).

PP -> AS (IN REF. 1).

I -> L (IN REF. 2).

Q -> R (IN REF. 2).

Q -> R (IN REF. 2).
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NONHELICAL REGION (NC4).
TRIPLE-HELICAL REGION (COL3).
NONHELICAL REGION (COL2).
TRIPLE-HELICAL REGION (COL2).
NONHELICAL REGION (NC2).
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J. Biol.
           REVISIONS TO C-TERMINUS.

MEDLINE=89380199; PubMed=2476437;

Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;

Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;

"The cloning and sequencing of alpha 1(VIII) collagen cDNAs demonstrate that type VIII collagen is a short chain collagen and contains triple-helical and carboxyl-terminal non-triple-helical domains similar to those of type X collagen.";

J. Biol. Chem. 264:16022-16029(1989).
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01-NOV-1991 (Rel. 20, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
Collagen alpha 1(X) chain precursor.
COL10A1.
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                                                                                                                                                 MEDIINE-89054019; PubMed=2461368;
Luvalle P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;
"The type X collagen gene. Intron sequences split the 5'-untran region and separate the coding regions for the non-collagenous terminal and triple-helical domains.";
J. Biol. Chem. 263:18378-18385(1988).
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                                                                                                                                                                                                                                                                                                                          Olsen
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X COLLAGEN IS
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P05997;
01-APR-1988
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HUMAN
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SEQUENCE
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PIR; A31896; A31896.
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Extracellular matrix; Connective
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InterPro; IPR000087; Collagen.
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SUBUNIT: HOMOTRIMER.

PIM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REFUNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAIN SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.

SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                        QDGPPQSP 333
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S; PR00007; COMPLEMNTC1Q.
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SM00110; C1Q; 1.
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HYDROXYLATION.
HYDROXYLATION.
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Pred. No. 0
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
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NONHELICAL REGION (
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DB 1

Indels 122;

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CREAR REPRESENTATION OF COLUMN AND ACCOUNT OF THE PROPERTY OF

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Collagen alpha
COL5A2.
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Weil D., Bernard M.P., Gargano S., Ra
"The pro alpha 2(V) collagen gene is
major fibrillar-forming collagens.";
Nucleic Acids Res. 15:181-198(1987).
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MEDLINE=89123368; PubMed=2914927;

Woodbury D., Benson-Chanda V., Ramirez F.;

Woodbury D., Benson-Chanda V., Ramirez F.;

"Amino-terminal propeptide of human pro-alpha 2(Y) collagen conforms to the structural criteria of a fibriliar procollagen molecule.";

J. Biol. Chem. 264:2735-2738(1989).
                                                                                                                                                                                                                                                                                  Michalickova K., Susic M., Willing M.C., Wer "Mutations of the alpha2(V) chain of type V assembly and produce Ehlers-Danlos syndrome Hum. Mol. Genet. 7:249-255(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94237164; PubMed=8181482;
MODIANE=94237164; PubMed=8181482;
MODIANE-Ameli M.; Rousseau J.C., Kleman J.P., Champliaud M.F.,
Boutillon M.M., Bernillon J., Wallach J.M., van der Rest M.;
"Diversity in the processing events at the N-terminus of type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                            Richards A.J.,
Burrows N.P.;
                                                                                                                                                                                                                   VARIANT EDS-II
PubMed=9783710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
MEDLINE=92239022; PubMed=1571108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  located on the long arm of Genomics 3:275-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE OF 398-1496 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                             PubMed=9425231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 288-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation of the alpha 3-chain of human type characterization by partial sequencing."; piol Chem. Hoppe-Seyler 373:69-75(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 208-227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89138450; PubMed=3224983;
Tsipouras P., Schwartz R.C., Liddell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1449-1496 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic
                                                                                                                                                                                                                                                                                                                                                                                                  SEASE
                                                                                                        Med. Genet.
                                                                                                                                                    single base mutation
                  FUNCTION: TYPE V COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
(FIBRILLAR FORMING COLLAGEN). IT IS A MINOR CONNECTIVE TISSUE
COMPONENT OF NEARLY UBIQUITOUS DISTRIBUTION. TYPE V COLLAGEN BINDS
TO DNA, HEPARAN SULFATE, THROMBOSPONDIN, HEPARIN, AND INSULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              distance of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٦.
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ha 2(V) chain p
                                                                                                           35:846-848 (1998)
                                                                                                                                                                                            Martin S.,
                                                                                                                                                                                                                                        ARG-960.
                                                                                                                                                                                                                                                                                                                                                                                                                                            221:987-995(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND 606-617.
ဝူ
                                                                                                                                                    in
TWO ALPHA 1(V)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrillar collagen
                                                                                                                                                                                                 Nicholls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor
                                                                                                                                                    COL5A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
                                                                                                                                                    causes
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human
                                                                                                                                                                                              A.C., Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramirez F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.C., Salkeld C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evolutionarily related
AND ONE
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alpha
                                                                                                                                                                                                                                                                                                            Wenstrup R.J., Cole
e V collagen impair m
ome type I.";
                                                                                                                                                    Ehlers-Danlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       loci, COL3A1 and COL5A2, 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type
                                                                                                                                                                                            J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V procollagen
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                                                                                                                                                    syndrome
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                                                                                                                                                                                                                                                                                                                                 e W.G.;
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GPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP--

169 500

QSPRG-: : ||| RGPRGDI

PGTLGPPGPVGERGAPGNRGF----

PGSDGLPGPKGAQGERGPVGSSGPKGSQ

GSFGRGG

554 273 ----DPTSNATSRGAE

217

GAV-PRKPVSEMPMERDRGAAHSLEPGKENLPG----

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9999999999999999999999999
Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J04478; AAA51859.1; --
EMBL; X04758; CAA28454.1; --
EMBL; M1718; AAA52058.1; --
PIR; A25374; A25374.
PIR; A25874; A25874.
PIR; A3017; A30017.
PIR; A31427; A31427.
                                            CONFLICT
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PROPEP
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VARIANT
                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                          Pfam; PF00093; vwc; 1. Pfam; PF01391; Collagen; 18. Pfam; PF01410; Collei; 1. ProDom; PD000007; Collagen; 5. ProDom; PD002078; Fib collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreemant (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                Disease
SIGNAL
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                                                                                                                                                                                                                                                    Extracellular matrix; Co
Glycoprotein; Collagen;
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000087;
InterPro; IPR000885;
InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew;
                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOST TISSUES AND TRIMERS OF ONE ALPHA 1(V), ONE ALPHA 2(V), AND ONE ALPHA 3(V) CHAINS IN PLACENTA.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

DISEASE: Defects in COL5A2 are a cause of Ehlers-Danlos syndrome gravis or type I (EDS-I), and Ehlers-Danlos syndrome mitis or type II (EDS-I). Ehlers-Danlos syndrome is a genetically and phenotypically heterogeneous connective-tissue disorder characterized by loose-jointedness and fragile, velvety, stretchable, bruisable skin that heals with peculiar 'cigarette-paper' scars. EDS-I and EDS-II are autosomal dominant traits.

SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                                                                                                                                                                                                                                                                                         SM00038; COLFI;
SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:2210; COL5A2
           Similarity
                                                                                                                                                                                                                                             mucacion
                                                                                                                                                                                                                                                                              PS01208; VWFC; 1.
                                                                                                                            1227
1227
290
290
293
294
608
614
                                              292
1418
1438
1460
1496
1496
 Conservative
                                             A
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1418
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1438
1460
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1496
297
290
293
293
614
                                                                                                                                                                                                                                                                                                                                                               , rib_collagen_C.
; VWF_C.
         7.7%;
29.1%;
                                              144720
                                                                                                                                                                                                                                                                   Connective
                                                                                                                                                                                                                                                     Signal;
                                                       /FTId=VAR 013588.
A -> P (IN REF. 6).
K -> T (IN REF. 3).
F -> Q (IN REF. 3).
E -> Q (IN REF. 4).
V -> A (IN REF. 4).
                                              ₹:
                                                                                                                                                   HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
 Score 142.5; DB
Pred. No. 0.051;
5; Mismatches
                                                                                                                          HYDROXYLATION.
G -> R (IN EDS-II).
                                                                                                                                                                                                         COLLAGEN ALPHA 2 (V
                                                                                                                                                                                                                                                                                                               ĵ.
                                                                                                                                                                                                                                                     tissue; Repeat; Hydroxylation;
Ehlers-Danlos syndrome;
                                              82827C17A8644F5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib
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(V)
 76;
                      μ,
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                       Length
                                              CRC64;
  Indels
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                         1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration
  43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
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  Gaps
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RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA18 HUMAN STANDARD,
P27658; Q96D07;
01-AUG-1992 (Rel. 23, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 1 (VIII) chain precursor (Endot
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                        EMBL; BC013581; AAH13581.1;
PIR; S15435; S15435.
Genew; HGNC:2215; COL8A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muragaki Y., Mattei M.-G., Yamaguchi N., Olsen B.R., "The complete primary structure of the human alpha 1 assignment of its gene (COLBAL) to chromosome 3."; Eur. J. Biochem. 197:615-622(1991).
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 8.
PRINTS; PR000007; COMPLEMNTC1Q.
ProDom; PD000007; Collagen; 1.
SMART; SM00110; ClQ; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal.
SIGNAL 1 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=91231001; PubMed=2029894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                              EMBL; X57527; CAA40748.1;
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                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                        InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MITTED (SEP-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION WITH ALPHA 2 (VIII) TYPE COLLAGENS.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
MISCELLANBOUS: FOUR CONSECTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE THE HIGH THERMAL STABILITY OF THIS REGION.

SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : || |
GDPGRPGEPGLPGARG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LTGNPGVQGPEGKLGPLGAPGEDGRPGPPGSIGIKGQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Endothelial collagen)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ninomiya Y.;
(VIII) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
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Best Local S
Matches 72
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                             CA26 MOUSE STANDARD; PRT; 1029 AA (002788; Q05505; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Collagen alpha 2(VI) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
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DOMAIN
                                                  MEDIINE=93143659; PubMed=8380980; Ibrahimi A., Bertrand B., Bardon Ailhaud G., Dani C.; Cloning of alpha 2 chain of type mouse development."; Biochem. J. 289:141-147(1993).
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                              COL6A2
                                                                                                                                                                                                                     SEQUENCE FROM N.A. Ibrahimi A., Bardo
STRAIN=C57BL/6;
                 SEQUENCE OF 266-600
                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                 SEQUENCE OF 266-1029 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417
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Pred. No. 0.02'
.6; Mismatches
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                                                                                           expression
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MEDLINE=91226374; PubMed=1709252; Constantinou C.D., Jimenez S.A.;

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Piam; Folls); College...

Pfam; PR01391; College...

PRINTS; PR00453; VWFADOMAIN.

SMART; SM00327; VWA; 3.

PROSITE; PS50234; VWFA; 3.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation;

Extracellular matrix; Connective tissue; Repeat; Hydroxylation;

PROFINIAL.

POTENTIAL.

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"Cloning and sequence analysis of cDNAs encoding the alpha 1, all and alpha 3 chains of mouse collagen VI.";

Biochem. J. 291:787-792(1993).

-i- FUNCTION: COLLAGEN VI ACTS AS A CELL-BINDING PROTEIN.

-i- SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(ALPHA 2(VI), AND ALPHA 3(VI).

-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADIPOSE TISSUE, LUNG, ADRENAL GLANDS AND OVARY. LOWER LEVELS IN TESTIS, TONGUE, SKI.

KIDNEY, HEART, INTESTINE AND SPLEEN. NO EXPRESSION IN SKELETAL MUSCLE OR LIVER.

-I- PTM: DPOI.1NTC AM MINISTERIA POR SPORTING AND SPECENTA POR SPORTING AND SPORTING AND SPECENTA POR SPORTING POR SPORTING POR SPORTING POR SPORTING POR SPORTING POR S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:88460; Col6a2.
InterPro; IPR000087; Collagen.
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X65582; CAA46541.1; -.
EMBL; X62332; CAA44206.1; -.
EMBL; Z18272; CAA79153.1; -.
EMBL; 106343; AAA37441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of cDNAs encoding the triple-helical domain of murine alpha 2 (VI) collagen chain and comparison to human and chick homologues. Use of polymerase chain reaction and partially degenerate oligonuclectide for generation of novel cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00092; vwa; 3.
Pfam; PF01391; Collagen; 4.
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GNDSL -> TGNDS (IN REF. 4)
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Best Local
                                                                                                     DOMAINS.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; I (SHOWN HERE) AND II; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DOWAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE DOMAIN (NC1) AT THEIR CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.

-!- PTM: PROLINES AT THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.
-!- PTM: PROLINES AT THE TRIPLE DISSITION OF THE TRIPLE-TIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-!- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTERMOLECULAR DISULFIDE BONDING. 12 OF THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                "The complete primary structure of a nematode alpha 2(IV) and the partial structural organization of its gene.";
J. Biol. Chem. 266:16149-16156(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Collagen alpha 2(IV) chain precursor.
Ascaris suum (Pig roundworm) (Ascaris lumbricoides)
Eukaryota, Metazoa, Nematoda; Chromadorea; Ascaridiae; Ascarididae; Ascaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA24 ASCSU
P27393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6253;
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                                                                                                                                                                                                                                                                                                                                  FUNCTION: COLLAGEN TYPE IV IS SPECIFIC FOR BASEMENT MEMBRANES SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) CHAIN TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH INTERMOLECULAR INTERACTIONS BETWEEN 78 DOMAINS AND BETWEEN NC:
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                                                                                                   COLLAGENS.
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Pred. No. 0.
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SEQUENCE OF 1065-1466 FROM N.A.
MEDLINE=85087944; PubMed=6096827;
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SEQUENCE FROM N.A.
TISSUE=Skin fibroblast;
MEDLINE=89350888; PubMed=2764886;
MEDLINE=80350888; PubMed=2764886;
MEDLINE=80350888; PubMed=2764886;
                                                                                                                              MEDLINE=89098346; PubMed=3211760;
Molymeux K., Dalgleish R.;
"Human type III collagen 'variant'
Nucleic Acids Res. 16:11833-11833 (
                                                                                                                                                                                                                                                             MEDLINE=80198282; PubMed=6246925; Seyer J.M., Mainardi C., Kang A.H.; Seyer J.M., Mainardi C., Kang Collagen: am (III)-CB5 from type III collagen of Biochemistry 19:1583-1589(1980).
                                                                                                                                                                                                                                                                                                                                      "Covalent structure of collagen: ami consecutive CNBr peptides from type Biochemistry 17:3404-3411(1978).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain of human type III procollagen. Diff from type I procollagen and conservation Biochem, J. 260:509-516(1989).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
      SEQUENCE OF 965-1;
MEDLINE=81208139;
                                           procollagen."
Nucleic Acids
                                                              Rosenbloom J., Myer
"Molecular cloning
                                                                                                                                                                                             Mankoo B.S., Dalgleish R.;
"Human pro alpha 1(III) collagen: cDNA
Nucleic Acids Res. 16:2337-2337(1988).
                                                                                                                                                                                                                             SEQUENCE OF 950-1466 FROM N.A. MEDLINE=88189827; PubMed=3357782;
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Seyer J.M., Kang A.H.;
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MEDLINE=77134724; Po
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"Structure of cDNA clones coding
 J.M.,
                                                                          H.R., Brinker J.M.,
bloom J., Myers J.C.
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                                            Res.
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  A.H.
             PubMed=7016180;
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MEDLINE=91045136; PubMed=2235526;

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in the triple-helical domain of type III procollagen are an
infrequent cause of aortic aneurysms.";
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MEDLINE=86187804; PubMed=3754462;
MISKULIN M., Dalyleish R., Kluve-Beckerman B., Rennard S.I.,
Tolstoshev P., Brantly M., Crystal R.G.;
Thuman type III collagen gene expression is coordinately modulated
with the type I collagen genes during fibroblast growth.";
with the type ISOllagen genes during fibroblast growth.";
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with aortic aneurysms.";
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VARIANT AORTIC ANEURYSM ARG-303,
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TISSUE=Placenta;
MEDLINE=88303360; PubMed=3405773;
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MEDLINE=91056145; PubMed=2243125;
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"Nucleotide sequence of a cDNA coding fo.
of human prepro alpha (III) collagen.";
Nucleic Acids Res. 16:7201-7201(1988).
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                                                                                                                                                                                                                                   86:1465-1473
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I procollagen (COL3A1) in a family
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VARIANT EDS-IV VAL-1077.
MEDLINE=91374480; PubMed=1895316;
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90037070; PubMed-2808425; Tromp G., Kuivaniemi H., Stolle C.A., I "Single base mutation in the type III E the codon for glycine 883 to aspartate Ehlers-Danlos syndrome IV."; J. Biol. Chem. 264:19313-19317(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  converts glycine 847 syndrome type IV. An mutation.";
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Tromp G., de Paepe A., Nuytinck L.,
"Substitution of valine for glycine
Ehlers-Danios syndrome type IV.";
Hum. Mutat. 5:179-181(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  produces mutant molecules with different causes Ehlers-Danlos syndrome type IV.", J. Med. Genet. 30:690-693(1993). [20]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A single base mutation in the gene for type III collagen (COL3) converts glycine 847 to glutamic acid in a family with Ehlers-DJ syndrome type IV. An unaffected family member is mosaic for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT EDS-IV GLU-1014.
MEDLINE=92316511; PubMed=1352273;
Richards A.J., Ward P.N., Narcisi
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J. Biol. Chem. 264:1349-1352(1989).
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                                                                                                                                                                                                                                                   Johnson
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                                                                                                                                                                                                                                                                                                    "Characterisation of a glycine to va
position 910 of the triple helical va
patient with Ehlers-Danlos syndrome
J. Med. Genet. 28:458-463(1991).
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 -GAPGHP-----GPP
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Yamaguchí N., Benya P.D., Van der Rust M., Ninomiya Y.;

Yamaguchí N., Benya P.D., Van der Rust M., Ninomiya Y.;

Yamaguchí N., Benya P.D., Van der Rust M., Ninomiya Y.;

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Yamaguchí N., Benya P.D., Van der Rust M., Ninomiya Y.;

Yamaguchí N., Benya P.D., Van der P.D., Van Hersen M., Ninomiya Y.;

Yamaguchí N., Benya P.D., Van der Rust Descentive M., Ninomiya Y.;

Yamaguchí N., Benya P.D., Van der Rust Descentive M., Ninomiya Y.;

Yamaguchí N., Ninomiya N., N., N
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Best Local :
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Glycoprotein; Cell adhesion; Collagen; Signal.
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Pfam; PF01391; Collagen; 8.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SN00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
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Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Eukaryota; Metazoa; Lagomorpha; Leporidae; Oryctolagus.
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01-NOV-1995 (Rel. 32, Last annotation update)
Collagen alpha i(VIII) chain precursor (Endothelial collagen).
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                                                                                                                                                                                                                                                                                                          RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Adacta K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchil P., Lewis S., Matsuo Y., Nikaido I., King B., Kochiwa H.,
RA Kuchil L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.

-!- SUBUNIT: WAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION WITH ALPHA 2 (VIII) TYPE COLLAGENS.
-!- TISSUE SPECIFICITY: HIGH LEVELS IN CALVARIUM, EYE & SKIN OF NEWBORN MICE, ALSO IN VARIOUS EPITHELIAL, ENDOTHELIAL AND MESENCHYMAL CELLS:
-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-!- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Alpha'l (VIII)-collagen gene transcripts encode a short-chain collagen polypeptide and are expressed by various epithelial, endothelial and mesenchymal cells in newborn mouse tissues."; Eur. J. Blochem. 207:895-902(1992).
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(200780; C992V4;
01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(VIII) chain precursor.
                                                                                                                                                                                                                                  Nature 409:685-690(2001-1- FUNCTION: MAJOR COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE-Kidney;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
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Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=1499564;
ta C., Inoue M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coshima
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Fukuda S.,
manaka I.,
Saito R.,
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Best Loca
Matches
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PROSITE; PRO1113; C10; 1.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal.

SIGNAL 28 BY SIMILARITY.

CHAIN 29 743 COLLAGEN ALPHA 1 (VIII) CHAIN.

DOMAIN 29 117 NONHELICAL REGION (NC2).

DOMAIN 118 571 TRIPLE-HELICAL REGION (COL1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:88463; Col8a1.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
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Pfam; PF01391; Collagen;
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Local &
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AEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGP---
                       GKPGQDGIPGQPGFPGGKGEQGLPGLPGPPGLPGVGKPGFPGPKGDRGIGGVPGVLGPR-
                                                                  PPGMHGPPGPVGLPGVGKPGVTGFPGPQGPLGKPGPPGEPGPQGLIGVPGVQGPPGMPGV
                                                                                         -PAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG----
                                                                                                              GPPGPHGLPGIGKPGGPGLPGQPGAKG-ERGPKGPPGLQGPKGEKGFGMPGLPGLKG
                                                                                                                                     G--AAHSL----EPGKENLPGDPTSNATSRGAEGPLPPPSM-----
                                                                                                                                                            GKPGPQGYPGIGKPGMPGMPGKPGAMGMPGAK-----GEIGPKGEIGPMGIPGPQ
                                                                                                                                                                                  TSDGT-----REGLESLQG--GVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDR 190
                                                                                                                                                                                                            LRGEQGPRGEPGPRGPPGP
                                                                                                                                                                                                                                VGGAQGRRCE----APPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIA 139
                                                                                                                                                                                                                                                       QQVPHMPLGKDGLSMGKEMPHMQYGKEYPHLPQYMKEIPPVPRMGKEVVPKKGKEVPLAS 115
                                                                                                                                                                                                                                                                                 ---PH----
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                                                                                                                                                                                                                                                                                                                                                     101;
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3; PS01112
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109
248
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                                                                                                                                                                                                                                                                                                                                                                                            NONHELICAL REGION (NC1).
C10.
G -> R (IN REF. 2).
H -> Y (IN REF. 1).
K -> KG (IN REF. 1).
P -> A (IN REF. 2).
P -> A (IN REF. 1).
P -> SR (IN REF. 1).
D -> H (IN REF. 1).
T -> P (IN REF. 2).
MPS -> NPF (IN REF. 1).
F584D85BD53897F4 CRC64;
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Pred.
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No. 0.034;
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                                             PGSFGRGGSLGLGG-GGGMGPRE
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         375
        GEKGPIGAPGMGG---
- PPGEPGLPGIPGPMGPPGAIGFPGPKGEGGVVGPQGPP
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PRESERVED BY LALE BERREAR BERR
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01-NOV-1995
01-NOV-1997
16-OCT-2001
                                                                                                                MEDLINE=97255959; PubMed=9101290;
Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI
associated collagen (type IX), and network-forming collagen
cause a spectrum of diseases of bone, cartilage, and blood
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 547-655 FROM N.A.

MEDLINE=92077285; PubMed=1743401;

Reichenberger E. Aigner T., von der Mark K., Stoeb H., B

Reichenberger E. Aigner T., von der Mark K., Stoeb H., B

"In situ hybridization studies on the expression of type
in fetal human cartilage.";
Dev. Biol. 148:562-572(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 561-666 FROM N.A. MEDLINE-9124388; PubMed-2037056; Apte S., Mattei M.-G., Ollsen B.R.; "Cloning of human alpha 1(X) collagen COL10A1 gene to the q21-q22 region of FEBS Lett. 282:393-396(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bertling 
"Genomic
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MEDLINE=92109659; PubMed=1764025;

Thomas J.T., Cresswell C.J., Rash B.,

Solomon B., Grant M.E., Boot-Handford

"The human collagen X gene. Complete
chromosomal localization.";
VARIANTS SMCD ASP-598 AND PRO-614.
MEDLINE=94136476; PubMed=8304336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92267014; PubMed=1587271;
Apte S.S., Seldin M.F., Hayashi M., Olsen B.:
"Cloning of the human and mouse type X collag-
The mouse type X collagen gene to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.
Beier F., Lammi
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                     REVIEW ON VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem.
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Reichenberger E., Beier
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Lammi M.B.,
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Schmid metaphyseal chondrodysplasia.";

J. Hum. Genet. 43:259-261(1998).

I. Hum. Genet. 43:259-261(1998).

I. FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.

I. SUBUNIT: HOMOTRIMER.

I. PYM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEAT UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

I. DISBASE: DEFECTS IN COLLIDAL ARE THE CAUSE OF SCHMID TYPE METAPHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED DISGREE OF THE OSSBUS SKELETON. THE CARDINAL FEATURES OF THE PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GPHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GPHENOTYPE ARE MILD SHORT STATURE.
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MEDLINE=99069781; PubMed=9852679;

Sawai H., Ida A., Nakata Y., Koyama K.;

"Novel missense mutation resulting in the substitution of tyrosine "Novel missense mutation resulting in the substitution of tyrosine cysteine at codon 597 of the type x collagen gene associated with
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MEDLINE 99057503; PubMed 9837818;
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Bonaventure J., Chaminade F., Maroteaux P.;
"Mutations in three subdomains of the carboxy-terminal reg
collagen type X account for most of the Schmid metaphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95181449; PubMed=7876225; Chan D., Cole W.G., Rogers J.G., Bateman J.F.; Chan D., Collagen multimer assembly in vitro is prevented by a Gly618 to Val mutation in the alpha 1(X) NC1 domain resulting in Schmid metaphyseal chondrodysplasia."; Di. Biol. Chem. 270:4558-4562(1995).
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Nakamura Y.;
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Hum. Mutat. 9:131-135(1997).
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ations in the N-terminal globular domain of the type X collagen
(CCL10A1) in patients with schmid metaphyseal
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EMBL; X72579; CAA51170.1; -.
EMBL; X72579; CAA51170.1; -.
EMBL; X72579; CAA51170.1; -.
EMBL; X72589; CAA51170.1; JCINED.
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DISEASE: DEFECTS IN COLLOAL ARE THE CAUSE OF SPONDYLOMETAPHYSEAL DISEASE; DISPEASIA (CMPRISES A HETEROGENEOUS GROUP OF HERITABLE SKELETAL DYSPLASIAS CHARACTERIZED BY MODIFICATIONS OF THE SKELETAL DODIES OF THE SPINE AND METAPHYSES OF THE TUBULAR BONES
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                                                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                                                        13,
                                                                                                      Score 140; DE
Pred. No. 0.03
3; Mismatches
                                                                                                                                                     G -> R.

/FTId=VAR 001840.

C -> R (IN SMCD).

/FTId=VAR_001841.
                                                                                                                                                                                                                                                                   CIQ.
                                                                                                                                                                                                                                                                                NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                     Disease mutation; POTENTIAL.
                                                                                                                                                                                                                          G -> E (IN SMCD).
/FTId=VAR 001838.
G -> R (IN SMCD).
                                                                                                                                                                                                                                                                                                                        COLLAGEN ALPHA 1(X)
                                                                                                                                                                                                             /FTId=VAR_001839
                                                                                                                   DB 1
                                                                                                                               <u>..</u>
                                                                                                         84;
                                                                                                                                                                                                                                                                                                                                                  Polymorphism.
                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                         Indels
                                                                                                                                   680;
                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
Loutstation -
                                                                                                         Gaps
                           270
                                                   129
 186
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8
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CAC2_HA
RESULT 47
CA1B_MOUSE
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                                                                                                                                                                                    Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAC2 HAECO
P16252;
01-AUG-1990
01-AUG-1990
15-JUN-2002
                                                                                                                                                                                                                                              Cuticle;
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAECO
                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shamansky L.M., Pratt D., Boisvenue R.J., Cox G.N., "Cuticle collagen genes of Haemonchus contortus and elegans are highly conserved.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Trichostrongyloidea; Haemonch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
15-UWN-2002 (Rel. 41, Last annotation
Cuticle collagen 2C (Fragment).
                                                                                                                                                                                                                                                                    Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                           EMBL; J04670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90136718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemonchus
                                                                                           110
                                                                                                                                                            176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDP--TSNATSRGAEGPLPPPSMPAVAGAAG
                                                                                                                                                                                                                                                                               nterPro;
                                              156
                                                                   290
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                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Parasitol 37:73-86(1989).

FUNCTION: NEWATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLES PUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

MISCELLANEOUS: THIS PROTEIN SHOWS 4 POTENTIAL TRIPLE-HELICAL REGIONS, WHICH CONVAIN GLYCINE AS EVERY THIRD AMINO ACID.

MISCELLANEOUS: IN ALL NEWATODE CUTICLE COLLAGENS, THE POLYPEPTIDE CHAINS ARE COMPLEXED MITHIN THE CUTICLE BY DISULPIDE BONDS AND CHAINS ARE COMPLEXED MITHIN THE CUTICLE BY DISULPIDE BONDS AND CHAINS ARE COMPLEXED TO THE CUTICULAR COLLAGEN FAMILY.
                                                                                                                GLALLLLGVAGAGGAMCWRRRRAKPSESRHPG----PGSFGRGGSLGLGGGGGGMGPREAE
                                             PGEKGPRGQDGHPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKGEMGYGAPG-----RPGERGLPGPQGPTGPSGPPGVGKRGENGVPGQPGIKGDRGF
                                                                   PGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPP
                                                                                                                                       IPIPPCKPCPQGRPGPPGPIGPPGEPGTPGNPGAPGNDAPPGPPGPKGPPGPPGKAGAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGEMGPIGPPGPQGPP
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                                                                                                                                                                                      50,
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                        Connective tissue; Repeat; Multigene family; Collagen
                                                                                                                                                                                                                                                                               1PR000087; Collagen.
                                                                                                                                                                                                                                   210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contortus (Barber pole worm).
Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2615789;
                                                                                                                                                                                                                                   19562 MW;
                                                                                                                                                                                              31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemonchidae; Haemonchinae; Haemonchus
                                                                                                                                                                                                            7.5%;
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                                                                                                                                                                                    ű
                                                                                                                                                                                    Score 139.5;
Pred. No. 0.01
5; Mismatches
                                                                                           PSEPLVPGPPGPPGPTGPEGPPGPNGAPGHPGAPGA
                                                                                                                                                                                                                                   E15FAA9A2DF3D74B CRC64;
                                             GNAGHPGQPGQPGPP 186
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                                                                                                                                                                               J.011;
75;
                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                          and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Caenorhabditis
                                                                                                                                                                                     Indels
                                                                                                                                                                                                           Length
                                                                                                                                                                                                            210;
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                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                         for commercial
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                                                                                                                                                                                    Gaps
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 ProDom; PD000007; Collagen; 1.
ProDom; PD002078; Fib collagen C;
SMART; SM00038; COLFF; 1.
SMART; SM000282; LamG; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                     EMBL;
                                                                  PF01410; COLFI;
PF02210; TSPN;
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Li Y., Lacerda D.A., Warman M.L., Beier D.R., Yoshioka H., Winomiya Y., Oxford J.T., Morris N.P., Andrikopoulos K., Ramirez F., Wardell B.B., Lifferth G.D., Teuscher C., Woodward Taylor B.A., Seegmiller R.E., Olsen B.R.;

"A fibrillar collagen gene, Collial, is essential for skeletal morphogenesis.",
Cell 80:423-430(1995).
Cell 80:423-430(1995).
CONTROLLING LATERAL GROWTH OF COLLAGEN IN FIBRILLOGENESIS BY CONTROLLING LATERAL GROWTH OF COLLAGEN IN FIBRILS.
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshioka H., Inoguchi K., Khaleduzzaman M., Andrikopoulos K., Ramirez F.; "Coding sequence and alternative splicing of collagen gene (Collai).", Genomics 28:337-340(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q61245; Q64047; (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) collagen alpha 1(XI) chain precursor. CCL11A1.
InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib collagen_C.
InterPro; IPR001991; Laminin_G.
InterPro; IPR001230; Prenyl_Site.
InterPro; IPR003129; TSPN.
                                                                                                                                                                                                         EMBL; D38162;
EMBL; S74574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95163095; PubMed=7859283;
Li Y., Lacerda D.A., Warman M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA1B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96015067; PubMed=8530046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                      send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(XI), ALPHA 2(XI), AND ALPHA 3(XI). ALPHA 3(XI) IS A POST-TRANSLATIONAL MODIFICATION OF ALPHA 1(II), ALPHA 1(IV) CAN ALSO BE FOUND INSTEAD OF ALPHA 3(XI)=1(II) (BY SIMILARITY).

OF ALPHA 3(XI)=1(II) (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPPIDE REPEATING PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPPIDE CHAINS.

DISEASE: DEFECTS IN COLLILAI ARE ASSOCIATED MITH CHONDRODYSPLASIA, AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY SKELETAL DEFECTS CAUSED BY ABNORMALITIES IN THE CARTILAGE OF LIMBS, RIBS, MANDIBLES AND THE CARTILAGE OF LIMBS, RIBS, MANDIBLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND TRACHEA.
SIMILARITY: BELONG
SIMILARITY: HIGH,
                                                                                                                                                                               MGI:88446; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181-198 FROM N.A.,
                                                                                                                                                                                                         BAA07367.1; -.
AAB33439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS. HIGH, TO ALPHA 1(V) AND ALPHA 3(V) CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1804
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Connective tissue; Repeat; Hydroxylation;

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RESULT 48
CA12_MOUSE
ID CA12_M
AC P28481
DT 01-DEC
DT 01-DEC
DT 16-OCT
DE CO11ag
GN CO12A1
OS MUS MU
CO12A1
OS MUS MU
CO12A1
OS MUS MU
CO12A1
OS MUS MU
RAN [1]
RN 
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Best Local :
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P28481;
01-DEC-1992
01-DEC-1992
16-OCT-2001
 structure,
J. Biol. C
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SITE
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CHAIN
PROPEP
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VARIANT
VARIANT
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SIGNAL
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
SEQUENCE FROM N.A.

MEDLINE=91358489; PubMed=1885613;

Metsaranta M., Toman D., de Crombrugghe B.,

"Mouse type II collagen gene. Complete nucle
structure, and alternative splicing.";

J. Biol. Chem. 266:16862-16869(1991).
                                                                                                                                                                                                              O1.DEC-1992 (Rel. 24, Created)
O1-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 1(II) chain precursor [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                 KGPQGKPGLAGLPGADGPPGHPGKEGQSGEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                   LGIALRGG-----GAADPPFCPHYEKVSGDYGHPVYIVQDGP--PQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA
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                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAMCWRRRAKPSESRHPG-PGSFGRGGSLGL-GGGGGMGPREAEPGE
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25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 139;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CROSSLINKING.
CROSSLINKING.
MISSING (IN SHORT ISOFORM).
LDRSERS -> SIEVRDR (IN CHONDRODYSPLASIA).
MISSING (IN CHONDRODYSPLASIA).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO-TERMINAL PROPEPTIDE (POTENTIAL).
COLLAGEN ALPHA 1(XI) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRIPLE-HELICAL REGION.
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                                                                                                                                                                                                                                                                                                         1459
                                                                                                                                                                                                                                                                                                                                                                                                 ----ALGPPGPQGP
                                    nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                       AA
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                                                        Vuorio E.;
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                                                                                                                                                                                                                    Chondrocalcin].
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                                     exon
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RESULT 49
CA2B_HUMAN
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Best Local :
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SEQUENCE
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PROPEP
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8 밁 Ş

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InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C
InterPro; IPR000085; Fib_collagen_C
InterPro; IPR001007; VWF_C.
Pfam; PF00093; vwc; 1.
Pfam; PF01391; Collagen; 18.
Pfam; PF01410; CoLFI; 1.
Pfam; PF01410; CoLFI; 1.
Pfam; PF0040007; Collagen; 3.
ProDom; PD000007; Collagen; 3.
ProDom; PD000078; Fib_collagen_C; 1
SWART; SM00038; VWC; 1.
SWART; SM00038; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: COLLAGEN TYPE II IS SPECIFIC FOR CARTILAGINOUS TISSUE:
-!- SUBUNIT: TRIMERS OF IDENTICAL ALPHA (III) CHAINS.
-!- PIM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-!- SIMILARITY: CONTAINS 1 VMFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Cartilage; Signal; Alternative splicing SIGNAL 1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE OF 1455-1459 FROM N.A.
MEDLINE=91274355; PubMed=2054384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Specific hybridization probes for mouse type I, II, collagen mRNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metsaranta M.,
                                                                                                                                                                                                                                                                                                  173 GGAVPRKFVSEMFMERDRGAAHSLEFGKENL-----PGD--FTSNATSRGAEGFLFFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:88452;
                                                                                                                           GGMGPREAEPGELGIA----LRG------GGAADPPFCPHYEKVSGDYGHPVYIVQDGP
                                                                                                                                                                                                                                                         GGAGPIGPPGERGAPGNRGF-----PGQDGLAGPKGAPGERGPSGLAGPKGANGDPGRPG
SGFQGLPGPPGPP
                                                                                                                                                                         EPGLPGARG:
                                                                                                                                                                                                             MPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP---
                                                                                  KGANGEPGKAGEKGLAGAPGLRGLPGKDGETGAAGPPGPSGPAGERGEQGAP----
                                           ------PQSPP
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1214
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                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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1186
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29
98
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                                                                                                                                                                    -LTGRPGDAGPQGKVGPSGAPGEDGRPGPPGPQGARGQPGVMGFPGP
                                                                                                                                                                                                                                                                                                                                                               7.5%;
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153
646
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                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                  Score 138.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                             TRIPLE-HELICAL REGION.

NONHELICAL REGION (C-TERMINAL).

Q -> R (IN SHORT ISOFORM).

MISSING (IN SHORT ISOFORM).

MF6CB4FA7C532E7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWFC
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CARBOXYL-TERMINAL PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO-TERMINAL
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                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  .09;
                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                             75;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 1459;
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                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                               -GSFGRGGSLGLGGG
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associated cause a spe
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SEQUENCE
                                                                                                                                                                           Melkoniemi M., Brunner H.G., Manouvrier S., Hennekam R., Superti-Furga A., Kaeaeriaeinen H., Pauli R.M., van Essen T., Warman M.L., Bonaventure J., Miny P., Ala-Kokko L., "Autosomal recessive disorder otospondylomegaepiphyseal dysplasia associated with loss-of-function mutations in the COLILA2 gene.", Am. J. Hum. Genet. 66:368-377(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lui V.C., Ng L.J., Sat E.W., Chech K.S.;
"The human alpha 2(XI) collagen gene (COL11A2): completion of coding information, identification of the promoter sequence, and precise localization within the major histocompatibility complex reveal overlap with the KE5 gene.";
Genomics 32:401-412(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             localization overlap with
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[5]
SEQUENCE OF 1-537 FROM N.A.
MEDLINE=96435918; PubMed=8838804;
Lui V.C., Ng L.J., Sat E.W., Chea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89340485; PubMed=2760050; Kimura T., Cheah K.S.E., Chan S.D.H., Lui V.C.H., Mattei M.-G., Kimura T., Cheah K.S.E., Chan S.D.H., Ninomiya Y., Olsen B.R.; van der Reet M., Ono K., Solomon E., Ninomiya Y., Olsen B.R.; "The human alpha 2(XI) collagen (COL11A2) chain. Molecular cloning of CDNA and genomic DNA reveals characteristics of a fibrillar collagen with differences in genomic organization."; J., Biol. Chem. 264:13910-13916(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhidkova N.I., Brewton R.G., Mayne R.; "Molecular cloning of PARP (proline/arginine-rich protein) from cartilage and subsequent demonstration that PARP is a fragment on the contract of the collagen alpha 2(XI) chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Cartilage;
MEDLINE=93314796; PubMed=8325374;
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Ala-Kokko L.;
Ala-Kokko L.;
COL11A2 gene
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P13942; 013273; 013271; 013272; 007751;
01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Collagen alpha 2(XI) chain precursor.
                                                                                                                                                                                                                                                                                                                                 PubMed=10677296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=96032717;
                                                                          Kuivaniemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Alternative mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                             ON VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   man COL11A2 gene structure inc
with the genes for the major
. Chem. 270:22873-22881(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                            chem. 2
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OCT-1998) to
H., Tromp G., Prockop D.J.,
in fibrillar collagens (types I, II, III
collagen (type IX), and network-forming
ectrum of diseases of bone, cartilage, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    730-1690 FROM N.A.
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hlajamaa T., Vandenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7721876;
                                                                        PubMed=9101290;
pmp G., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mayne R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           indicates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dicates that the gene has fibrillar collagens.":
                                                                                                                                                                                                                                                                                                                                                                                                                                    the variable region llagen chains.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prockop
III, and XI), fibri
ing collagen (type )
, and blood vessels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
                     fibril-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 m human
of the
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otospondylomegaepiphyseal dysplasia accompanied by severe hearing loss.

syndrome. DISEASE: Defects in

COL11A2 are the

cause of autosomal recessive (OSMED), a skeletal dysplasia. The phenotype overlaps that o

Lagia hat of

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CONTROLLING LATERAL GROWTH OF COLLAGEN II FIBRILS.

-ISUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(XI),
ALPHA 2(XI), AND ALPHA 3(XI) ALPHA 3(XI) IS A POST-TRANSLATIONAL
MODIFICATION OF ALPHA 1(II). ALPHA 1(V) CAN ALSO BE FOUND INSTEAD
OF ALPHA 3(XI)=1(II).

-I- ALTERNATIVE PRODUCTS: 8 isoforms; 1 (shown here), 2, 3, 4, 5, 6, 7
and 8; may be produced by alternative splicing. They lack exons 6,
7 or 8 or a combination of these exons.
-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPFIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-I- PTM: A DISULFIDE-BONDED PEPTIDE CALLED PROLINE/ARGININE-RICH
PROTEIN OR PARP IS RELEASED PROM THE AMINO TERMINUS DURING
EXTRACELIULAR PROCESSING AND IS SUBSEQUENTLY RETAINED IN THE
CARTILAGE MATRIX FROM WHICH IT CAN BE ISOLATED IN SIGNIFICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20047768; PubMed=10581026;
McGuirt W.T., Presad S.D., Griffith A.J., Kunst H.P.M., Gree
Shpargel K.B., Runge C., Huybrechte C., Mueller R.F., Lynch
King M.-C., Brunner H.G., Cremers C.W.R.J., Takanosu M., Li
Arita M., Mayne R., Prockop D.J., Van Camp G., Smith R.J.H.,
"Mutations in COLI1A2 cause non-syndromic hearing loss (DFNA)
Nat. Genet. 23:413-419(1999).

Nat. Genet. 23:413-419 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pihlajamaa T., Prockop D.J., Faber J., Winterpacht A., Zabel B., Giedion A., Wiesbauer P., Spranger J., Ala-Kokko L.; "Heterozygous glycine substitution in the CCLI1A2 gene in the ori patient with the Weissenbacher-Zweymueller syndrome demonstrates identity with heterozygous OSMED (nonocular Stickler syndrome).", Am. J. Med. Genet. 80:115-120(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95163096; PubMed=7859284;
Vikkula M., Mariman E.C.M., Lui V.C.H., Zhidkov
Vikkula M., Mariman B.C.M., Lui V.C.H., Zhidkov
Goldring M.B., van Beersum S.E.C., de Waal Malo
van den Hoogen F.H.J., Ropers H.-H., Mayne R.,
Olsen B.R., Warman M.L., Brunner H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [13]
VARIANTS DFNA13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COL11A2, the gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT STL3 940-GLY--PRO-948 DEL.
PubMed=9506662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic mapping
ligament of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robin N.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Stickler syndrome without
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AMOUNTS.

DISEASE: Defects in COLLIA2 are the cause of Stickler syndrome type 3 (STL3). It is an autosomal dominant disorder characterized by oro-facial, auditory and skeletal manifestations, such as midfacial hypoplasia, cleft palate, osteoarthritis, and sensorineural hearing loss. Differently from Stickler syndrome type 1 and 2, no ocular involvement is observed. This disorder is also referred to as Stickler-like syndrome or non-ocular Stickler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pediatr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutat.
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S., Otterud
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alpha-2(XI)
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posterior lor
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chain of type
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Best Local S
Matches 64
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InterPro; IPR000885; Fib collagen_C.
InterPro; IPR000885; Fib collagen_C.
InterPro; IPR001791; Laminin G.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR003129; TSPN.
Pfam; PF01410; COLF1; 1.
Pfam; PF01410; COLF1; 1.
Pfam; PF02210; TSPN; 1.
ProDom; PF0000077; Collagen; 1.
ProDom; PF0000077; Collagen; 1.
ProDom; PF0000078; Fib_collagen_C; 1.
SMART; SM00038; COLF1; 1.
SMART; SM00038; COLF1; 1.
SMART; SM00282; LamG; 1.
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EMBL; U32169; AAC50215.1; -.
EMBL; U32169; CAAC50215.1; -.
EMBL; AL031228; CAA20240.1; -.
EMBL; L11987; AAA35498.1; -.
EMBL; U41987; AAA352034.1; -.
EMBL; U41069; AAC17464.1; JOINED.
EMBL; U41066; AAC17464.1; JOINED.
EMBL; U41067; AAC17464.1; JOINED.
EMBL; U41067; AAC17464.1; JOINED.
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                   310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autosomal dominant skeletal disorders (Stickler and Marshall syndromes) but can be distinguished by disproportionately short limbs and lack of ocular involvement.

DISEASE: Defects in COLIIA2 are the cause of Meissenbacher-
Zweymueller syndrome (MZS), an autosomal dominant disorder allelic with STL3 and OSMED. It is also referred to as heterozygous OSMED.

DISEASE: Defects in COLIIA2 are the cause of autosomal dominant DISEASE: Defects in COLIIA2 are the cause of autosomal dominant nonsyndromic sensorineural deafness type 13 (DFNA13). Affected individuals experience progressive hearing loss beginning in the second to fourth decades, eventually making use of amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATABASE: NAME=Hereditary hearing loss homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE=Gene page;
WWW="http://www.uia.ac.be/dnalab/hhh/hhhgenes.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A32645; A32645
w; HGNC:2187; CC
HYEK-VSGDYGHPVYIVQDGPP
                                                  -EQGEKGDRGIPGPQGSPGQKGEMGIPGASGPIGP-GGPPGLPGPAGPKGAKGATGPGGP
                                                                                                                                                                                                GSEGRQGG----KGAK-----GDPGAIGAPGKTGPVGP----AGPAGKPGPDGLR
                                                                                                                                                                                                                                   GLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRK--PVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601868;
                                                                                                                           GLPGSVGQQGRPGATGQAGPPGPVGPPGLPGLRGDAGAKGEKGHPGLIGLIGPPG-----
                                                                                                                                                                 GDPTS----
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                                                                                    RRRAKPSESRHPGP-GSFGRGGSLGL-GGGGGMGPREAEPGELGIA-LRGGGAADPPFCP
                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                             -NATSR-GAEGPLPPPSMPAVAGAAGGLALL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COL11A2.
                                                                                                                                                                                                                                                                                        7.5%;
                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                     Score 138.5; DB 1;
Pred. No. 0.11;
8; Mismatches 71;
                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                       49;
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Ol-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 2(IV) chain precursor (Lethal LET-2 OR CLB-1 OR FOIG12.5.
Caenorhabditis elegans.
Caenorhabditis elegans, Nematoda, Chromadorea, Rhabditidae, Peloderinae, Caenorhabditis.
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This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foe entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sibley M.H., Graham P.L., von Mende N., Kramer J.M.; "Mutations in the alpha 2(IV) basement membrane collagen gene of Caenorhabditis elegans produce phenotypes of differing severities."; EMBO J. 13:3278-3285(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIDJEY M.H., Johnson J.J., Mello C.C., Kramer J.N. "Genetic identification, sequence, and alternativ Caenorhabditis elegans alpha 2(IV) collagen gene. J. Cell Biol. 123:255-264(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Collagen type IV is specific for basement membranes Vital for embronic development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guo X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90008929; PubMed=2793871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94320591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The two Caenorhabditis elegans basement membrane (type IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94012964; PubMed=7691828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS: 2 isoforms; I/a (shown here) and II/b; ar produced by alternative splicing.

Droduced by alternative splicing.

Droduced by alternative splicing.

Droduced by alternative splicing.

Droduced by alternative splicing.

I spredominant in spredominant in embryos and isoform II is predominant in the larvae and adults.

Domain: Alpha CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE G-X-Y REDEATS IN THE COCCENTRAL TRIPLE-HELICAL DOMAIN (WHICH CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) COUTYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH
                                                                                                                                             PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 THESE, LOCATED IN THE NCI DOMAIN, ARE CONSERVED IN ALL KNOWN TY. IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERMOLECULAR INTERACTIONS BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGEKGVQGPPGHP----GPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are located on separate chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kramer J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8045258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM
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Best Local Similarity 29.4%;
Matches 64; Conservative
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EMBL; Z22964; CAA80537.1; -.
EMBL; J05066; AAA27989.1; -.
EMBL; U22327; AAA6431Z.1; ALT_SEQ.
EMBL; U53342; AAA96215.1; -.
EMBL; U53342; AAA96216.1; -.
EMBL; U53342; -.
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1118 DGLPGRDG-----LPGVPGQKGDLG-----QSGQP 1142
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                                                                                                                                          1017 NGLPGEKGEAGPAARDGQKGDAGLPGQP-----GLRGPQGPSGLPGVPGFKGE-----
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ProDom; PD003923; ProcollagnC4; 2.
SMART; SM00111; C4; 2.
Hydroxylation; Connective tissue;
Alternative splicing; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPeg; F01G12.5a; CE04334.
WormPeg; F01G12.5b; CE04335.
InterPro; IPR000087; Collagen.
InterPro; IPR001442; ProcollagnC4.
Pfam; PF01391; Collagen; 23.
Pfam; PF01431; C4; 2.
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                                  LGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPP 330
                                                                          TGLPGYG---
                                                                                                          LGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSL-----GLGGGGGMGPREAEPGE 292
                                                                                                                                                                              -----AAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 239
                                                                                                                                                                                                                DGGLPGLPGLNGPKGEPGVPGMPGTPGMK-----GNGGLPGLPGRDGLSGVPGMKGDRGF 1016
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                                                                      ---QPGQPGEKGLPGIPGKAGRQGAPGSPGQDGLPGPPGMKGESGYPGQ 1117
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TRIPLE-HELICAL REGION (NC1).
NONHELICAL REGION (NC1).
NON 1632 (BY SIMILARITY).
OR 1635 (BY SIMILARITY).
BY SIMILARITY.
OR 1747 (BY SIMILARITY).
BY SIMILARITY.
OR 1750 (BY SIMILARITY).
OR 1750 (BY SIMILARITY).
BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
GDLGSVGPPGPPGPPRFTGSGSIVGPRGNFGEKGDK -> G
DIGAMGPAGPPGPTASTMSKGTTIGFKGDLGEKGEK (IN
                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                             Score 138; DB 1; Length 1758;
Pred. No. 0.12;
2; Mismatches 76; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
COLLAGEN ALPHA 2(IV) CHAIN.
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97EE3F3DBB2D2AC5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                       E (IN MN114; 73% LETHAL).

E (IN MN126; 100% LETHAL).

E (IN MN109; 37% LETHAL).

R (IN MN103 AND MN151; 96% LETHAL).

R (IN MN103; 50% LETHAL).

R (IN MN102; 50% LETHAL).

E (IN MN102; 100% LETHAL).

E (IN MN129; 100% LETHAL).

E (IN MN143; 100% LETHAL).

E (IN MN143; 100% LETHAL).

R (IN G30; 90% LETHAL).

R (IN G30; 90% LETHAL).

R (IN G30; 90% LETHAL).

D (IN MN147; 7% LETHAL).
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                                                                                                                                            1064
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Search completed: February 11, 2003, 12:03:55 Job time: 25.5409 secs